



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179881

TO: Christian Fronda
Location: 2d78 / 2c70
Thursday, March 02, 2006
Art Unit: 1652
Phone: 571-272-0929
Serial Number: 10 / 014774

From: Jan Delaval
Location: Biotech-Chem Library
Remsen 1a51
Phone: 571-272-2504

jan.delaval@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

179881

From: Fronda, Christian
Sent: Friday, February 17, 2006 9:56 AM
To: STIC-Biotech/ChemLib
Subject: RE: Score Over Length Sequence Searches for Serial NO. 10/014,774

Importance: High

Sorry for my mistake. The correct case is Serial No. 10/014,774.

I have made the corrections to the original email below. Thank you.

Christian L. Fronda
Art Unit 1652
Office REM 2D78
Mailbox REM 2C70
(571)272-0929

RECEIVED
FEB 17 2006
(STIC)

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Friday, February 17, 2006 9:50 AM
To: Fronda, Christian
Subject: RE: Score Over Length Sequence Searches for Serial NO. 10/014,744

There is no valid CRF for this serial number, please provide us with another valid serial number. Thank you

-----Original Message-----

From: Fronda, Christian
Sent: Friday, February 17, 2006 9:39 AM
To: STIC-Biotech/ChemLib
Subject: Score Over Length Sequence Searches for Serial NO. 10/014,774
Importance: High

Score over Length Searches for Serial No. 10/014,774

1. Please do a score over length search on SEQ ID NO: 1, minimum length 10, maximum length 1036 , with a score/length value = 1 (i.e. % match = 100)

Please search against nucleic acid commercial, PGPub, issued, and interference databases.

SAVE 50 Hits, if available.

2. Please do a score over length search on SEQ ID NO: 3, minimum length 10, maximum length 970 , with a score/length value = 1 (i.e. % match = 100)

Please search against nucleic acid commercial, PGPub, issued, and interference databases.

SAVE 50 Hits, if available.

Searcher: [Signature]
Searcher Phone: 22504
Date Searcher Picked up: 2/28/06
Date completed: 3/2/06
Searcher Prep Time: 20
Online Time: 150

Type of Search
NA# 18 AA#
S/L: ✓ Oligomer: ✓
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIS:
LEXIS/NEXIS:
SEQUENCE SYSTEM: ✓
WWW/Internet:
Other (Specify):

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 2, 2006, 10:50:59 ; Search time 1 Seconds
(without alignments)
3.181 Million cell updates/sec

Title: US-10-014-774-1
Perfect score: 1036
Sequence: 1 cccgtgacggcttgag.....gagaaaaa.....1036

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 1535 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 10
Maximum DB seq length: 1036

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : us-10-014-774-1.sl.rge4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1036	100.0	1036	1 AX045359	ACCESSION:AX045359
2	487.5	47.1	499	1 AX045372	ACCESSION:AX045372

ALIGNMENTS

RESULT 1
AX045359
LOCUS AX045359
DEFINITION Sequence 1 from Patent WO0066733.
ACCESSION AX045359
VERSION AX045359.1 GI:11343859
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
D'Azzo, A., Bongiovanni, A. and Nastasi, T.
Protein specific for cardiac and skeletal muscle
TITLE Patent: WO 0066733-A 1 09-NOV-2000;
JOURNAL ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
FEATURES
source
1. .1036
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"

Query Match 100.0%; Score 1036; DB 1; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCCTGTTGCACGGCTTGGAGATGGCTCTCCCTCCGAAACAGTAGGACTGGGTGCCCCAC	60
DB	1	CCCTGTTGCACGGCTTGGAGATGGCTCTCCCTCCGAAACAGTAGGACTGGGTGCCCCAC	60
QY	61	GGAGCCCTGGCGCCGAGAGCCCTCCACCCGCTTCCACCAAGTGCATGGAGCCCAACA	120
DB	61	GGAGCCCTGGCGCCGAGAGCCCTCCACCCGCTTCCACCAAGTGCATGGAGCCCAACA	120
QY	121	TCGCGATGAGCCCTCAGGAAACGCGAGCCACACCCGCTGGAGAGTTTCCGCCACCGTGTGT	180
DB	121	TCGCGATGAGCCCTCAGGAAACGCGAGCCACACCCGCTGGAGAGTTTCCGCCACCGTGTGT	180
QY	181	GCTTCAGTCTGTAGCCCTCGCCCGCCGAGGATTTCTAGTGGAATTCAGGAAAG	240
DB	181	GCTTCAGTCTGTAGCCCTCGCCCGCCGAGGATTTCTAGTGGAATTCAGGAAAG	240
QY	241	AGCTGGGCTGGTGGGGCACCCTACGCTTGGCCCTGAGCCGCTCTGGATCCGCCAGTCTGG	300
DB	241	AGCTGGGCTGGTGGGGCACCCTACGCTTGGCCCTGAGCCGCTCTGGATCCGCCAGTCTGG	300
QY	301	CCGCTGTACCCGAGTTTCTACTGCTGACTTTGGTTCAGCTTGGCCACAGTTGGGTCTTCG	360
DB	301	CCGCTGTACCCGAGTTTCTACTGCTGACTTTGGTTCAGCTTGGCCACAGTTGGGTCTTCG	360
QY	361	CTATCACACGCGCCACCAACCGTGTGCCCGGGAGGTCACACCAAGCGGAGCGAGCGG	420
DB	361	CTATCACACGCGCCACCAACCGTGTGCCCGGGAGGTCACACCAAGCGGAGCGAGCGG	420
QY	421	TCCCGAGTGTCCCAAGCCCTACTGTTGAAACCTATCTCGGCATCAGACAGTTCGAA	480
DB	421	TCCCGAGTGTCCCAAGCCCTACTGTTGAAACCTATCTCGGCATCAGACAGTTCGAA	480
QY	481	TTCCCGGAGCGCTGTGGTGGCGCGAGCGCGGCTTTATAGCCACCTCTTAGATC	540
DB	481	TTCCCGGAGCGCTGTGGTGGCGCGAGCGCGGCTTTATAGCCACCTCTTAGATC	540
QY	541	AGCTCTATGAAACAAACGCTGCTCTCTCAGCGCGCGGAGCGGCTTGGGTGTCTCT	600
DB	541	AGCTCTATGAAACAAACGCTGCTCTCTCAGCGCGCGGAGCGGCTTGGGTGTCTCT	600
QY	601	TCTGCCCGGTGAGGATGGGACCGCGGACATCATCATCAACCGGAGGACATGG	660
DB	601	TCTGCCCGGTGAGGATGGGACCGCGGACATCATCATCAACCGGAGGACATGG	660
QY	661	GCCCTAGCGCCGGGGGCTGCGAGTGTCTAGCCCTCTAGCTGTGGTAGATGTTTG	720
DB	661	GCCCTAGCGCCGGGGGCTGCGAGTGTCTAGCCCTCTAGCTGTGGTAGATGTTTG	720
QY	721	CTTCCACCAAGAGCGTGTCTGTTCCAGCTGGAGTATGGCTTGCATCTCTGCAGACTC	780
DB	721	CTTCCACCAAGAGCGTGTCTGTTCCAGCTGGAGTATGGCTTGCATCTCTGCAGACTC	780
QY	781	TGTGCGGACTAGTATCCAGAAAGGGTGTACACAGGCTGGCCATTAATGTGCTCACC	840
DB	781	TGTGCGGACTAGTATCCAGAAAGGGTGTACACAGGCTGGCCATTAATGTGCTCACC	840
QY	841	TGCCCAAAAGGACTGAAGGACTTCTCAAGTACCAATGAACGAATCAACGCTGTCTGG	900
DB	841	TGCCCAAAAGGACTGAAGGACTTCTCAAGTACCAATGAACGAATCAACGCTGTCTGG	900
QY	901	CCACGAGCAAGTCCCGGGTGGCGGCTTCTAGAGAGTGGTAGTCTGAGG	960
DB	901	CCACGAGCAAGTCCCGGGTGGCGGCTTCTAGAGAGTGGTAGTCTGAGG	960
QY	961	TGCTGCGCAGCTCACAATCAGGGCTGGAAATAAATAGAGCGGATGTGAGTCTGAGA	1020
DB	961	TGCTGCGCAGCTCACAATCAGGGCTGGAAATAAATAGAGCGGATGTGAGTCTGAGA	1020
QY	1021	AAAAAAAAAAAAAAAAAAAA 1036	
DB	1021	AAAAAAAAAAAAAAAAAAAA 1036	

```

RESULT 2
AX045372/c
LOCUS      AX045372      499 bp      DNA      linear      PAT 24-NOV-2000
DEFINITION Sequence 14 from Patent WO0066733.
ACCESSION  AX045372
VERSION     AX045372.1  GI:11343862
KEYWORDS
SOURCE      Mus sp.
ORGANISM    Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS    D'Azzo, A., Bongiovanni, A. and Nastasi, T.
TITLE       Protein specific for cardiac and skeletal muscle
JOURNAL     Patent: WO 0066733-A 14 09-NOV-2000;
            ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
FEATURES
Source      1..499
            /organism="Mus sp."
            /mol_type="unassigned DNA"
            /db_xref="taxon:10095"

Query Match      47.1%; Score 487.5; DB 1; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 265 GTCTTGGCCTGACCGCTCTGGATCCCGCAGTCTGGCGGCTGTACCCGAGTTTTCACCTGC 324
Db 499 GTCTTGGCCTGACCGCTCTGGATCCCGCAGTCTGGCGGCTGTACCCGAGTTTTCACCTGC 440

Qy 325 CTGACTTGGTCAGCCTTGGCCACAGTTGGGTCTTCGCTATCACACGCCACCAACCGTG 384
Db 439 CTGACTTGGTCAGCCTTGGCCACAGTTGGGTCTTCGCTATCACACGCCACCAACCGTG 380

Qy 385 TGCCCCGGGAGGTCAACAGAGCGGAGCGGTCGCCAGTGGTCCCCAGCCCTAC 444
Db 379 TGCCCCGGGAGGTCAACAGAGCGGAGCGGTCGCCAGTGGTCCCCAGCCCTAC 320

Qy 445 TGGTTGAACCTATCTCGCATCAGCAGTTCCGAATTCGCCGGACCGTCTGGTGGGCC 504
Db 319 TGGTTGAACCTATCTCGCATCAGCAGTTCCGAATTCGCCGGACCGTCTGGTGGGCC 260

Qy 505 GCAGCCGGCCAGGCTTTATAGCCACCTCTTTAGATCAGCTCTATGAACAAACGTCGTGC 564
Db 259 GCAGCCGGCCAGGCTTTATAGCCACCTCTTAGATCAGCTCTATGAACAAACGTCGTGC 200

Qy 565 CTCCTACAGCGCGCGGAGCGGCTTGGGTCTCTCTTCTGCCCGCGTGAGGATGGGACCG 624
Db 199 CTCCTACAGCGCGCGGAGCGGCTTGGGTCTCTCTTCTGCCCGCGTGAGGATGGGACCG 140

Qy 625 CCGACATGCATCATCATCAACGGGAGGACATGGGCCCTAGCGCCCGGGGGCTGCCAG 684
Db 139 CCGACATGCATCATCATCAACGGGAGGACATGGGCCCTAGCGCCCGGGGGCTGCCAG 80

Qy 685 CTGCTCAGCCCTCTACGCTGTGTAGATGTGTGTTCACCAAGAGCGT-GCGTCTG 743
Db 79 CTGCTCAGCCCTCTACGCTGTGTAGATGTGTGTTCACCAAGAGCGTGTGCGTCTG 20

Qy 744 GTCCAGCTGGAGTATGGCT 762
Db 19 GTCCAGCTGGAGTATGGCT 1

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Search completed: March 2, 2006, 10:51:01
Job time : 2 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:53:08 ; Search time 4 Seconds
(without alignments) 3.741 Million cell up

Title: US-10-014-774-1
Perfect score: 1036
Sequence: 1 cctgtttgcacgqcttggag.....gagaaaaaaaaaaaaaa 1036

Scoring table: IDENTITY_NUC
Gapop 10.0 : Gapext 0.5

Searched: 18 seqs, 7222 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 10
Maximum DB seq length: 1036
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 18 summaries

Database : us-10-014-774-1.sl.rst4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1006.6	97.2	1014	1	AK004524	ACCESSION: AK004524
C 2	660.6	63.8	684	1	C0039719	ACCESSION: C0039719
C 3	632.4	61.0	634	1	BE650303	ACCESSION: BE650303
C 4	442.2	42.7	457	1	BE956589	ACCESSION: BE956589
C 5	439.2	42.4	445	1	BY1262946	ACCESSION: BY1262946
C 6	430.2	41.5	443	1	AW1241138	ACCESSION: AW1241138
C 7	399.4	38.4	402	1	BY267664	ACCESSION: BY267664
C 8	366.8	35.4	384	1	BY105284	ACCESSION: BY105284
C 9	358.3	34.6	376	1	BY670130	ACCESSION: BY670130
C 10	334.4	32.3	336	1	AW125078	ACCESSION: AW125078
C 11	325.4	31.4	335	1	BE955244	ACCESSION: BE955244
C 12	320.8	31.0	326	1	BY781925	ACCESSION: BY781925
C 13	253.4	24.5	255	1	CL631771	ACCESSION: CL631771
C 14	249.8	24.1	257	1	CG487097	ACCESSION: CG487097
C 15	243.8	23.5	251	1	CG479214	ACCESSION: CG479214
C 16	224	21.6	228	1	EX632311	ACCESSION: EX632311
C 17	199	19.1	200	1	CX214893	ACCESSION: CX214893
C 18	188.6	18.2	195	1	AV022299	ACCESSION: AV022299

ALIGNMENTS

RESULT 1	AK004524	AK004524	1014 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK004524	Mus musculus 18-day embryo whole body cDNA, RIKEN full-length				
DEFINITION		enriched library, clone:119009E12 product:hypothetical SOCS				
		domain, C-terminus of STAT-inhibitors containing protein, full				
		insert sequence.				
ACCESSION	AK004524					
VERSION	AK004524.1	GI:12835749				
KEYWORDS		HTC; CAP trapper.				

cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
XhoI. Host: SOLR.
FEATURES
 source
 Location/Qualifiers
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 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="PANTOM,DB:1190009E12"
 /db_xref="taxon:10090"
 /clone="1190009E12"
 /tissue_type="whole body"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="18-day embryo"
 18..875
 /note="unnamed protein product; hypothetical SOCS domain,
 C-terminus of STAT-inhibitors containing protein
 (InterPro|IPR001496, evidence: InterPro)
 putative"
 /codon_start=1
 /protein_id="BAB23346.1"
 /db_xref="GI:12835750"
 /translation="MADPSEHVLGVGPRSPARPEPPTRPHQVHGAINRMDPSGTRAT
 RVSFANGVCFREPLAPGVFLVEIEKEELGWCGHLRLGLTALDPASLAAPVPEFSLP
 DLVSLGHSWFAITHRNVRPREGQPEAEAVSPGQALLAVEPLRIEOPRIIPDRILV
 GRSRPGLYSHLLDLYEQNVLPPTARRSRLGVLPFCPRDGTADMHIIINGEDMGPSAR
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 GLKDFCKYE"
 987..992
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 1014
 /note="putative"

polyA_signal
987..992
polyA_site
1014
/note="putative"

Query Match 97.2%; Score 1006.6; DB 1; Length 1014;
Best Local Similarity 93.6%; Pred. No. 0.0018;
Matches 1009; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GTTTCACGGCTTGAGATGGCTGCTCCCTCGAACACAGTAGGACTGGGTGCCACCGAG 64
Db 2 GTTTCACGGCTTGAGATGGCTGATCTCCCTCGAACACAGTAGGACTGGGTGCCACCGAG 61
Qy 65 CCTCTGCGCGCCAGAGCCCTCCACCGCTTCCCAAGTGTGATGGAGCCACATCCG 124
Db 62 CCTCTGCGCGCCAGAGCCCTCCACCGCTTCCCAAGTGTGATGGAGCCACATCCG 121
Qy 125 CATGGACCCCTCAGGAACGGAGCCACACCGTGGAGATTTTCGCCACCGTGTGCTT 184
Db 122 CATGGACCCCTCAGGAACGGAGCCACACCGTGGAGATTTTCGCCACCGTGTGCTT 181
Qy 185 CAGTCTGAGCCCTTGGCCCGCCGCGAGTATTTCTAGTGAATTTGAGGAAAAGAGCT 244
Db 182 CAGTCTGAGCCCTTGGCCCGCCGCGAGTATTTCTAGTGAATTTGAGGAAAAGAGCT 241
Qy 245 GGGCTGGTGGGGGACCTTACGCTTTGGCTGACCGCTCTGATCCCGCAGTCTGGCGCG 304
Db 242 GGGCTGGTGGGGGACCTTACGCTTTGGCTGACCGCTCTGATCCCGCAGTCTGGCGCG 301
Qy 305 TGTATCCCGAGTTTTCAGTCCCTGACTTGGTTCAGCCTTTGGCCACAGTTGGGTCTTCGCTAT 364
Db 302 TGTATCCCGAGTTTTCAGTCCCTGACTTGGTTCAGCCTTTGGCCACAGTTGGGTCTTCGCTAT 361
Qy 365 CACAGCCACACAAACCGTGTGCGCCGGGAAGGTCAACAGAGCGAGCGGTGCC 424
Db 362 CACAGCCACACAAACCGTGTGCGCCGGGAAGGTCAACAGAGCGAGCGGTGCC 421
Qy 425 CAGTGGTCCCAAGCCCTTACTGGTTGAACCCCTATCTGCGCATCCAGAGTTCGGAATCC 484
Db 422 CAGTGGTCCCAAGCCCTTACTGGTTGAACCCCTATCTGCGCATCCAGAGTTCGGAATCC 481
Qy 485 CCGGGAACCGTCTGGTGGCGCGACCGCGCCAGGGCTTTATAGCCACCTCTTTAGATCAGCT 544
Db 482 CCGGGAACCGTCTGGTGGCGCGACCGCGCCAGGGCTTTATAGCCACCTCTTTAGATCAGCT 541
Qy 545 CTATGAACAAACAGTGTGCTGCTCCTCTACAGCGCGCCGAGCGCGTGTGGGTCTTCTCTCTG 604

Db 542 CTATGAACAAACAGTGTGCTCCTCTACAGCGCGCCGAGCGGTGTGGGTCTTCTCTCTG 601
Qy 605 CCCCCGTGAGGATGGGACCGCGACATGCAATCATCATCAACCGGGAGGACATGGGCC 664
Db 602 CCCCCGTGAGGATGGGACCGCGACATGCAATCATCATCAACCGGGAGGACATGGGCC 661
Qy 665 TAGCGCCCGGGGCTGCCAGCTGCTCAGCCCTCTAGGCTGTGGTGTAGATGTGTGCTTC 724
Db 662 TAGCGCCCGGGGCTGCCAGCTGCTCAGCCCTCTAGGCTGTGGTGTAGATGTGTGCTTC 721
Qy 725 CACCAAGAGCGTGGTCTGGTCTCAGCTGGAGTATGGCTTGCACATCTCTGCAGACTCTGTG 784
Db 722 CACCAAGAGCGTGGTCTGGTCTCAGCTGGAGTATGGCTTGCACATCTCTGCAGACTCTGTG 781
Qy 785 CCGACTAGTGAATCAGGAAGGGTGGTACACAGGCTGGCCATTGATGTGCTCCACCTGCC 844
Db 782 CCGACTAGTGAATCAGGAAGGGTGGTACACAGGCTGGCCATTGATGTGCTCCACCTGCC 841
Qy 845 CAAAGACTGAAGGACTTCTGCAAGTACGAATGAACGAATGAACGCTGTCTGTGGCCAC 904
Db 842 CAAAGACTGAAGGACTTCTGCAAGTACGAATGAACGAATGAACGCTGTCTGTGGCCAC 901
Qy 905 CAGAGCAAAAGTCCCGGCTGGTGGCCCTGCCTCTAGAGAAGTGGCTAGTCTGAAGCTGGT 964
Db 902 CAGAGCAAAAGTCCCGGCTGGTGGCCCTGCCTCTAGAGAAGTGGCTAGTCTGAAGCTGGT 961
Qy 965 CGCACAGCTCACAATCAGGCTGGAAATAAATAGACCGGATGGGATGTTCTG 1017
Db 962 CGCACAGCTCACAATCAGGCTGGAAATAAATAGACCGGATGGGATGTTCTG 1014

RESULT 2
CO039719/c
LOCUS
DEFINITION
 684 bp mRNA linear EST 10-JUN-2004
 UI-M-BH2.1-apr-e-06-0-UI-sl NIH BMAP_M S3.1 Mus musculus cDNA clone
 UI-M-BH2.1-apr-e-06-0-UI 3', mRNA sequence.
ACCESSION
 CO039719
VERSION
 CO039719.1 GI:48578618
KEYWORDS
 EST.
SOURCE
 Mus musculus (house mouse)
ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
 1 (bases 1 to 684)
AUTHORS
 NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
 Unpublished (1999)
COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rc@mail.nih.gov
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 <http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pyX-3
 POLYA=Yes.
FEATURES
 source
 Location/Qualifiers
 1..684
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH2.1-apr-e-06-0-UI"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH_BMAP_M S3.1"
 /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NIH_BMAP_M S3.1 library is a subtracted library of a

series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M.S3.1, NIH_BMAP_M.S2, NIH_BMAP_M.S1. The subtracted library (NIH_BMAP_M.S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M.S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M.S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M.S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG_TISSUE=olfactory bulbs
TAG_LIB=UI-M-BH2.1
TAG_SEQ=CATGG

Query Match		63.8%;	Score 660.6;	DB 1;	Length 684;
Best Local Similarity		98.4%;	Pred. No. 0.075;	11;	Indels 0; Gaps 0;
Matches 666;		Conservative 0;	Mismatches 11;	Indels 0;	Gaps 0;
QY	351	TGGGCTCTTCGCTATCACACGCGCACCAACCGTGTGCCCCGGGAAGGTCACACGAGCG	410		
DB	677	TGGCTTCGNTATCACACGCGCACCAACCGTGTGCCCCGGGAAGGTCACACGAGCG	618		
QY	411	GAGGACGCGTCCCGAGTGGTCCCCAAGCCCTACTGTTGAACCTATCTGGCATCGAG	470		
DB	617	GAGGACGCGTCCCGAGTGGTCCCCAAGCCCTACTGTTGAACCTATCTGGCATCGAG	558		
QY	471	CAGTTCGCAATTCCTCCGCGGACCGTCTGGTGGCGCGCAGCGCGGCTTTATAGCCAC	530		
DB	557	CAGTTCGCAATTCCTCCGCGGACCGTCTGGTGGCGCGCAGCGCGGCTTTATAGCCAC	498		
QY	531	CTCTTAGATCAGCTCTATGAACAAACGTCGTCCCTCTTACAGCGCGCGGAGCGCTTG	590		
DB	497	CTCTTAGATCAGCTCTATGAACAAACGTCGTCCCTCTTACAGCGCGCGGAGCGCTTG	438		
QY	591	GGTGTCTCTTCTGCCCCCGTGAGATGGACCGCGCATGCAATCATCATCAACGGG	650		
DB	437	GGTGTCTCTTCTGCCCCCGTGAGATGGACCGCGCATGCAATCATCATCAACGGG	378		
QY	651	GAGGACATGGGCTTAGCGCCCGGGGCTGCGCTGCTGCTTACAGCGCGCTTACGCTGGTA	710		
DB	377	GAGGACATGGGCTTAGCGCCCGGGGCTGCGCTGCTGCTTACAGCGCGCTTACGCTGGTA	318		
QY	711	GATGTGTTTGTCTTCCACCAAGAGCGTGGTCTGGTCCAGCTGGAGTATGGCTTGCATCT	770		
DB	317	GATGTGTTTGTCTTCCACCAAGAGCGTGGTCTGGTCCAGCTGGAGTATGGCTTGCATCT	258		
QY	771	CTGCAGACTCTGTGCGGACTAGTGATCCAGAGAGGGTGGTACACAGGCTGGCCATGAT	830		
DB	257	CTGCAGACTCTGTGCGGACTAGTGATCCAGAGAGGGTGGTACACAGGCTGGCCATGAT	198		
QY	831	GTGTCTCACCTGCGCAAGGACTGAAGGACTTCTGCAAGTACGATGACGATGACGCG	890		
DB	197	GTGTCTCACCTGCGCAAGGACTGAAGGACTTCTGCAAGTACGATGACGATGACGCG	138		
QY	891	CTGTCTGCGCCACAGCAAGTCCCGGTGGTGGCGCTTCCCTCTAGAGAGTGGCT	950		
DB	137	CTGTCTGCGCCACAGCAAGTCCCGGTGGTGGCGCTTCCCTCTAGAGAGTGGCT	78		
QY	951	AGTCTGAAGCTGGTCCGACAGCTCACAATCAGGCGCTGGAAATATAATAGACCGCATGTGA	1010		
DB	77	AGTCTGAAGCTGGTCCGACAGCTCACAATCAGGCGCTGGAAATATAATAGACCGCATGTGA	18		

QY 1011 TGTTCTGAGAAAAAAA 1027

DB 17 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 3

BE650303

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BE650303

UI-M-BH2.1-apr-e-06-0-UI.r1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone

UI-M-BH2.1-apr-e-06-0-UI.5', mRNA sequence.

BE650303

UI-M-BH2.1-apr-e-06-0-UI.r1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone

UI-M-BH2.1-apr-e-06-0-UI.5', mRNA sequence.

BE650303

UI-M-BH2.1-apr-e-06-0-UI.r1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone

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BE

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 Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 1 AGAGCCCTCCACCCGCTTCCCAAGTGCATGAGCCCAACATCCGCATGAGCCCTC 60

Qy 137 AGGAACGGGAGCCACACGCTGGAGAGTTTCGCCACAGGTGTGTCTTCACTGTAGTCCAGCC 196
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 Db 121 CCTGGCCCGCCGACAGTATTCTAGTGGAAATTTAGAGAAAAGAGCTGGCTGTGCGG 180

Qy 257 GCACCTAGCTTGTGGCTGACCGCTCTGGATCCCGCAGTCTGGCCGCTGTACCCGAGTT 316
 Db 181 GCACCTAGCTTGTGGCTGACCGCTCTGGATCCCGCAGTCTGGCCGCTGTACCCGAGTT 240

Qy 317 TTCACTGGCTGACTTGTGCTTGGCTTGGCCACAGTTGGGTCTTCGCTATCAACGCCACCA 376
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Qy 377 CAACCGTGTGCCCGGAGAGTCAACAGAGCGAGGAGCAGCGTCCCGAGTGTGCCCA 436
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Qy 437 AGCCCTACTGTGTAACCCCTATCTGCGCATCGAGCAGTTCGGAATCCCGGGACCGTCT 496
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Qy 497 GGTGGCGCGAGCGCCGAGGCTTTATAGCACCTCTTAGATCAGCTCTATGAACAAA 556
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Qy 557 CGTGTGCTCTTACAGCGCCGAGCGCTGTGGGTCTCTTCTGCTGCTGAGGAGGA 616
 Db 481 CGTGTGCTCTTACAGCGCCGAGCGCTGTGGGTCTCTTCTGCTGCTGAGGAGGA 540

Qy 617 TGGGACCGCCGACATGCATCATCATCAACGGGAGGACATGCGCCCTAGCGCCCGGG 676
 Db 541 TGGGACCGCCGACATGCATCATCATCAACGGGAGGACATGCGCCCTAGCGCCCGGG 600

Qy 677 GCTGCCAGCTCTCAGCCCTCTACGCTGTGGTA 710
 Db 601 GCTGCCAGCTCTCAGCCCTCTACGCTGTGGTA 634

RESULT 4
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 VERSION BE956589.1 GI:10601286
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 457)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 8889548
 CONTACT Contact: Chin, H
 NATIONAL INSTITUTE OF MENTAL HEALTH
 6001 EXECUTIVE BLVD. ROOM 7N-7190, MSC 9643, BETHESDA, MD
 20892-9643, USA
 TEL: 301 443 1706

Pax: 301 443 9890
 Email: mES@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to verify it as a clone from the
 olfactory bulb tissue cDNA Library Preparation: M.B. Soares Lab
 Clone distribution: Researchers may obtain BMAP cDNA clones from
 RESEARCH GENETICS. It should be noted that Bento Soares is
 generating a small number of additional specialized non-redundant
 arrays of BMAP cDNAs whose availability will be considered under
 appropriate and limited collaborative arrangements
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES
 source

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BG2-bbm-a-08-0-UI"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH BMAP MSC S1"
 notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NIH BMAP MSC S1 library is a subtracted library derived
 NIH BMAP MSC N. NIH BMAP MSC N was made from mouse spinal
 cord tissue. For a detailed description of the library
 from which this clone was derived, please visit our web
 site at brainest.eng.uiowa.edu.
 TAG TISSUE=olfactory-bulbs
 TAG LIB=NIH BMAP MSC_S1
 TAG SEQ=CATGG"

Query Match 42.7%; Score 442.2; DB 1; Length 457;
 Best Local Similarity 97.8%; Pred. No. 0.93; Indels 0; Gaps 0;
 Matches 447; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 570 ACAGCGCGCGAAGCGCTTGGGTGTCTCTTCTGCCCCCGTGAGGATGGACCGCGAC 629
 Db 457 ACAGCGCGCGAAGCGCTTGGGTGTCTCTTCTGCCCCCGTGAGGATGGACCGCGAC 398

Qy 630 ATGCACATCATCATCAACGGGAGGACATGCGCCCTAGCGCCCGGGGCTGCCAGTGTCT 689
 Db 397 ATGCACATCATCATCAACGGGAGGACATGCGCCCTAGCGCCCGGGGCTGCCAGTGTCT 338

Qy 690 CAGCCCTCTACGCTGTGGTGTAGATGTTTGTCTTCCACCAAGAGCGTGTGGTCCAG 749
 Db 337 CAGCCCTCTACGCTGTGGTGTAGATGTTTGTCTTCCACCAAGAGCGTGTGGTCCAG 278

Qy 750 CTGGAGTATGGTGGCCATCTCTGCAGACTCTGTGCGGACTAGTGTATCCAGAGAGGGTG 809
 Db 277 CTGGAGTATGGTGGCCATCTCTGCAGACTCTGTGCGGACTAGTGTATCCAGAGAGGGTG 218

Qy 810 GTACACAGGCTGGCCATTGATGTCTCCACCTGCCCAAGGACTGAGGACTTCTGCAAG 869
 Db 217 GTACACAGGCTGGCCATTGATGTCTCCACCTGCCCAAGGACTGAGGACTTCTGCAAG 158

Qy 870 TAGCAATGAACGAATGAAGCCCTGTCTGTGGCCACACAGAGCAAGTCCCGGGTGGTCCGC 929
 Db 157 TAGCAATGAACGAATGAAGCCCTGTCTGTGGCCACACAGAGCAAGTCCCGGGTGGTCCGC 98

Qy 930 CCTGCTCTTAGAGAAGTGGCTAGTCTGAAGCTGGTCCGACAGCTCACAATCAGGGTGGGA 989
 Db 97 CCTGCTCTTAGAGAAGTGGCTAGTCTGAAGCTGGTCCGACAGCTCACAATCAGGGTGGGA 38

Qy 990 AATAAATAGAGCCGATGTGGATGTTCTGAGAAAAAAA 1026
 Db 37 AATAAATAGAGCCGATGTGGATGTTCTGAGAAAAAAA 1

RESULT 5
 BY262946/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BY262946 445 bp mRNA linear EST 10-DEC-2002
 BY262946 RIKEN full-length enriched, visual cortex Mus musculus
 cDNA clone K330317106 5', mRNA sequence.
 BY262946
 BY262946.1 GI:26444458
 EST.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 445)

REFERENCE
 AUTHORS

Okazaki, Y., Furuta, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nishida, I., Osato, N., Saito, R., Suzuki, H., Yamashita, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

TITLE
 JOURNAL
 PUBMED
 COMMENT

12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
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 Normalization and subtraction of cap-trapper-selected cDNAs to
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 encyclopedia: real-time sequence clustering for construction of a
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 cDNA library was prepared and sequenced in Mouse Genome
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Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michela Fagiolini and Takao K. Hensch (
 Laboratory for Neuroonal Circuit Development Brain Science Institute
 RIKEN 2-1 Hirooawa, Wako-shi, Saitama 351-0198 Japan) whose
 assistance we gratefully acknowledge. Please visit our web site
 (http://genome.gsc.riken.go.jp) for further details.

FEATURES
 Location/Qualifiers
 1. 445
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="K330317106"
 /tissue_type="visual cortex"
 /clone_lib="RIKEN full-length enriched, visual cortex"

Query Match 42.4%; Score 439.2; DB 1; Length 445;
 Best Local Similarity 99.3%; Pred. No. 0.99; 3; Indels 0; Gaps 0;
 Matches 441; Conservative 0; Mismatches 0;

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 Db 445 TGGCCCCAGGAGCCCTGCGGGCCAGAGCCCTCCACCCGCTTCCACCAAGTGCATGG 386
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 Db 325 CGGTGTGTCTTCACTGTGAGCCCTGGCCCGCCGAGGATTTCTAGTGGAAATGA 266
 QY 233 GGAAGAGAGCTGGCTGGTGGCGGACCTACGCTTGGCCCTGACCGCTCTGGATCCCGC 292
 Db 265 GGAAGAGAGCTGGCTGGTGGCGGACCTACGCTTGGCCCTGACCGCTCTGGATCCCGC 206
 QY 293 CAGTCTGGCCGCTGTACCCCGAGTTTTCAGTCCCTGACTTGTGTGAGCTTGGCCACAGTTG 352
 Db 205 CAGTCTGGCCGCTGTACCCCGAGTTTTCAGTCCCTGACTTGTGTGAGCTTGGCCACAGTTG 146
 QY 353 GGTCTTGTCTATACACGCGACCAACCGTGTCCCGGGAGGTCAACAGAGCCGA 412
 Db 145 GGTCTTGTCTATACACGCGACCAACCGTGTCCCGGGAGGTCAACAGAGCCGA 86
 QY 413 GCGAGCGTCCCGAGTGTCCCGAGCCCTACTGTTGAACCTATCTGCGCATCGAGCA 472
 Db 85 GCGAGCGTCCCGAGTGTCCCGAGCCCTACTGTTGAACCTATCTGCGCATCGAGCA 26
 QY 473 GTTCCGAATTCCTCCGGGACCGTCT 496
 Db 25 GTTCCGAATTCCTCCGGGACCGTCT 2

RESULT 6
 AW124138/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AW124138 443 bp mRNA linear EST 22-OCT-1999
 UI-M-BH2.1-apr-e-06-0-UI.sl NIH RWAP M_S3.1 Mus musculus cDNA clone
 UI-M-BH2.1-apr-e-06-0-UI.3', mRNA sequence.
 AW124138
 AW124138.1 GI:6099668
 EST.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 443)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED

Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 8889548

COMMENT

Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: m8st@mail.nih.gov

The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized olfactory bulbs library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

Source

Location/Qualifiers

1. 443

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-BH2.1-apr-e-06-0-UI"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NIH BMAP M_S3.1"

/note="Vector: p7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI: The

NIH_BMAP_M_S3.1 library is a subtracted library of a

series, ultimately derived from a mixture of individually

tagged normalized libraries from ten regions of the mouse

brain (cerebellum, brain stems, olfactory bulbs,

hypothalamus, cortex, amygdala, basal ganglia, pineal

gland, striatum, hippocampus) after a series of

subtractions to reduce the representation of cDNAs from

which ESTs had already been generated. The following

serially subtracted libraries were generated in this

process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1.

The subtracted library (NIH_BMAP_M_S3.1) was constructed

as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S2

clones from which 3' ESTs had been derived was used as a

driver in a hybridization with the NIH_BMAP_M_S2 library

in the form of single-stranded circles. The remaining

single-stranded circles (subtracted library) was purified

by hydroxyapatite column chromatography, converted to

double-stranded circles and electroporated into DH10B

bacteria (Life Technologies) to generate the

NIH_BMAP_M_S3.1 library. This procedure has been

previously described (Bonaldo, Lennon and Soares, Genome

Research 6:791-806, 1996)

TAG_TISSUE=olfactory-bulbs

TAG_LIB=NIH_BMAP_M_S3.1

TAG_SEQ=CATGG

Query Match 41.5%; Score 430.2; DB 1; Length 443;

Best Local Similarity 98.2%; Pred. No. 1.1;

Matches 435; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

584 CCGCTTGGGTGTTCTCTTCGCCCCCGTGAGGACCGCCGACATGCATCATCAT 643

443 CCGCTTGGGTGTTCTCTTCGCCCCCGTGAGGACCGCCGACATGCATCATCAT 384

644 CAACGGGAGGACATGGGCGCTAGCGCCGGGGCTGCCAGCTCTCAGCCCTCTACGC 703

383 CAACGGGAGGACATGGGCGCTAGCGCCGGGGCTGCCAGCTCTCAGCCCTCTACGC 324

704 TGTGGTAGATGTTGTTGTTCCACCAAGAGCGTGCCTTCCAGCTGGAGTATGCTT 763

323 TGTGGTAGATGTTGTTGTTCCACCAAGAGCGTGCCTTCCAGCTGGAGTATGCTT 264

QY 764 GCCATCTCTGCAGACTCTGTGCCGACTAGTGATCCAGAGAGGGTGGTACACAGGCTGGC 823
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QY 824 CATTGATGTGCTCCACTGCGCCCAAGAGACTGAAGGACTTCTGCAAGTACGAATGAACGAA 883
Db 203 CATTGATGTGCTCCACTGCGCCCAAGAGACTGAAGGACTTCTGCAAGTACGAATGAACGAA 144
QY 884 TGAACCGCTGTCTGTGGCCACACAGCAAGTCCCGGTGGTGGCCCTGCCTCTTAGAGA 943
Db 143 TGAACCGCTGTCTGTGGCCACACAGCAAGTCCCGGTGGTGGCCCTGCCTCTTAGAGA 84
QY 944 AGTGGCTAGTCTCAAGCTGTGTCACAGCTCACAATCAGGCTGGAATAAATAGAGCCG 1003
Db 83 AGTGGCTAGTCTCAAGCTGTGTCACAGCTCACAATCAGGCTGGAATAAATAGAGCCG 24
QY 1004 ATGTGATGTTCTTGAGAAAAA 1026
Db 23 ATGTGAAAAA 1

RESULT 7

BY267664/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

MUS MUSCULUS (house mouse)

MUS MUSCULUS

MUS MUSCULUS

MUS MUSCULUS

MUS MUSCULUS

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TITLE

JOURNAL

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michela Fagioli and Takao K. Hensch (
 Laboratory for Neuronal Circuit Development Brain Science Institute
 RIKEN 2-1 Hirosawa Wako-shi, Saitama 351-0198 Japan) whose
 assistance we gratefully acknowledge. Please visit our web site
 (<http://genome.gsc.riken.go.jp>) for further details.
 Location/Qualifiers
 1. 402

FEATURES
source

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="K430018111"
 /tissue type="visual cortex"
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 342 GGTATTTCTAGTGAAATTTGAGGAAAAGAGCTGGGCTGGTCCGGGACCTACGCTTTGG 283
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RESULT 8
 BY105284

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISMREFERENCE
AUTHORS

BY105284 384 bp mRNA linear EST 07-DEC-2002
 BY105284 RIKEN full-length enriched, pooled tissues, adult spleen,
 etc. Mus musculus cDNA clone K630160C04 5', mRNA sequence.
 BY105284
 BY105284.1 GI:26215901
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 384)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaado, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
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 Analysis of the mouse transcriptome based on functional annotation
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 Nature 420, 563-573 (2002)
 1246851

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>
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 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES		REFERENCE	
source		AUTHORS	
Location/Qualifiers			
1. 384			
/organism="Mus musculus"			
/mol_type="mRNA"			
/db_xref="taxon:10090"			
/clone="K630160C04"			
/clone_lib="RIKEN full-length enriched, pooled tissues, adult spleen, etc."			
/notes="(dev_stage=adult,tissue_type=spleen,sex=male), (dev_stage=adult,tissue_type=kidney,sex=male), (dev_stage=adult,tissue_type=testis,sex=male), (dev_stage=adult,tissue_type=thymus,sex=male), (dev_stage=adult,tissue_type=heart,sex=male), (dev_stage=adult,tissue_type=colon,sex=male), (dev_stage=adult,tissue_type=stomach,sex=male), (dev_stage=adult,tissue_type=liver,sex=male), (dev_stage=13 days embryo,tissue_type=whole body,sex=mix), (dev_stage=14 days embryo,tissue_type=whole body,sex=mix), (dev_stage=16 days embryo,tissue_type=whole body,sex=mix), (dev_stage=17 days embryo,tissue_type=whole body,sex=mix), (dev_stage=15 days pregnant, adult,tissue_type=amion,sex=female), (dev_stage=10 days neonate,tissue_type=brain,sex=mix), (dev_stage=10 days neonate,tissue_type=thymus,sex=mix), (dev_stage=10 days neonate,tissue_type=heart,sex=mix)"			
Query Match			
Best Local Similarity 99.2%; Score 366.8; DB 1; Length 384;			
Matches 368; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	1	CCCTGTTGCACGGCTGGAGATGCTGCTCCCTCCGAACACGTTAGGACTGGTGGCCAC	60
Db	14	CCCTGTTGCACGGCTGGAGATGCTGCTCCCTCCGAACACGTTAGGACTGGTGGCCAC	73
Qy	61	GGAGCCCTGGCGCCAGAGCCCTCCACCCGCTTCCACCAAGTCAGTGAGCCCAACA	120
Db	74	GGAGCCCTGGCGCCAGAGCCCTCCACCCGCTTCCACCAAGTCAGTGAGCCCAACA	133
Qy	121	TCCGCTAGGACCCCTCAGGAACGCGAGCCACACGCGTGGAGAGTTTCGCCACCGTGTG	180
Db	134	TCCGCTAGGACCCCTCAGGAACGCGAGCCACACGCGTGGAGAGTTTCGCCACCGTGTG	193
Qy	181	GCTTCAGTCGTGAGCCCTGGCCCGCCCGCAGGATTTCTAGTGGAAATTGAGGAAAAG	240
Db	194	GCTTCAGTCGTGAGCCCTGGCCCGCCCGCAGGATTTCTAGTGGAAATTGAGGAAAAG	253
Qy	241	AGCTGGGCTGGTGGGCGACCTACGTCTTGCGCTGACCGCTCTGGATCCGCGCAGTCTGG	300
Db	254	AGCTGGGCTGGTGGGCGACCTACGTCTTGCGCTGACCGCTCTGGATCCGCGCAGTCTGG	313
Qy	301	CCGCTGTACCCGAGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
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Qy	361	CTATCACACGC 371	
Db	374	CTATCACACGC 384	
RESULT 9			
BY670130			
LOCUS			
DEFINITION			
BY670130 RIKEN full-length enriched, 14.5 days embryo df/df			
Ratke's pouches Mus musculus cDNA clone K820011E02 3', mRNA			
sequence.			
BY670130			
VERSION			
BY670130.1 GI:27050464			
KEYWORDS			
EST.			
SOURCE			
Mus musculus (house mouse)			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1. (bases 1 to 376)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusci,V., Ciothia,C., Corbani,L.E., Cousins,S., Dalla,E., Drgani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hitokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawai,H., Kawasawa,Y., Kedziercki,R.M., King,B.L., Konagaya,A., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagasawa,T., Petrovsky,N., Pillai,R., Pavan,W.J., Pertea,G., Pesole,G., Numata,K., Okido,T., Pavan,W.J., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,K., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wanlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor,MI 48109-0638 USA) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

1. 376

/organism="Mus musculus"

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gscc.riken.jp, URL:<http://genome.gsc.riken.jp/>

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

FEATURES

source

Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=yes.

FEATURES

Source

1. .336
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/db_xref="taxon:10090"
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/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH BMAP M.S3.1"
/notes="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NIH BMAP M.S3.1 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH BMAP M.S3.1, NIH BMAP M.S2, NIH BMAP M.S1. The subtracted library (NIH BMAP M.S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH BMAP M.S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH BMAP M.S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH BMAP M.S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_TISSUE=prefrontal-cortex
TAG_LIB=NIH_BMAP_M.S3.1
TAG_SEQ=GCNCA"

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Matches	335;	Conservative	0;	Mismatches	1;
Indels	0;	Gaps	0;		
Qy	699	TACGCTGTGGTAGATGTTTGTTCACCAAGAGCGTGGTCTGGTCCAGCTGGAGTAT	758		
Db	336	TACGCTGTGGTAGATGTTTGTTCACCAAGAGCGTGGTCTGGTCCAGCTGGAGTAT	277		
Qy	759	GGCTTGCATCTTCGACAGCTCTGCGGACTAGTATCCAGAGAGGTTGTACACAGG	818		
Db	276	GGCTTGCATCTTCGACAGCTCTGCGGACTAGTATCCAGAGAGGTTGTACACAGG	217		
Qy	819	CTGGCCATTGATGCTCCACTGCGCCAAAGAGCTTGAAGGACTTCTGCAAGTACGAATGA	878		
Db	216	CTGGCCATTGATGCTCCACTGCGCCAAAGAGCTTGAAGGACTTCTGCAAGTACGAATGA	157		
Qy	879	ACGAATGAACGCTGTCTGTGGCCACAGAGCAAAAGTCCCCGGTGGTGGCCCTCCCTCT	938		
Db	156	ACGAATGAACGCTGTCTGTGGCCACAGAGCAAAAGTCCCCGGTGGTGGCCCTCCCTCT	97		
Qy	939	AGAGAAGTGGCTAGTCTGAAGCTGCTCCACAGCTCAANTCAGGGCTGGAAATAAATAG	998		
Db	96	AGAGAAGTGGCTAGTCTGAAGCTGCTCCACAGCTCAANTCAGGGCTGGAAATAAATAG	37		
Qy	999	AGCCCATGTGGATGTTCTGAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA	1034		
Db	36	AGCCCATGTGGATGTTCTGAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA	1		

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/db_xref="taxon:10090"
/clone="K820011E02"
/tissue_type="Rathke's pouches"
/dev_stage="14.5 days embryo df/df"
/clone_lib="RIKEN full-length enriched, 14.5 days embryo df/df Rathke's pouches"
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Best Local Similarity 98.9%; Pred. No. 2.5;
Matches 370; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 647 CGGGAGACATGGCCCTAGCGCCGGGGCTGCCAGCTGCTCAGCCCTCTACGCTGT 706
Db 1 CGGGAGACATGGCCCTAGCGCCGGGGCTGCCAGCTGCTCAGCCCTCTACGCTGT 60
Qy 707 GGTAGATGTTGTTCTTCCACCAAGAGCGTGGTCTGGTCCAGCTGGAGTATGCTTGGC 766
Db 61 GGTAGATGTTGTTCTTCCACCAAGAGCGTGGTCTGGTCCAGCTGGAGTATGCTTGGC 120
Qy 767 ATCTCTGAGACTCTGTGCGCACTAGTATCCAGAGAGGTTGTACACAGCTGGCCAT 826
Db 121 ATCTCTGAGACTCTGTGCGCACTAGTATCCAGAGAGGTTGTACACAGCTGGCCAT 180
Qy 827 TGATGTCTCCACCTGCCCAAGGACTGAAGGACTTCTGCAAGTACGAATGAACGAATGA 886
Db 181 TGATGTCTCCACCTGCCCAAGGACTGAAGGACTTCTGCAAGTACGAATGAACGAATGA 240
Qy 887 ACGCTCTGTGTGGCCACAGAGCAAGTCCCCGGT-GGTGGCCCTGCTTACAGAGAG 945
Db 241 ACGCTCTGTGTGGCCACAGAGCAAGTCCCCGGTGGTGGTGGCTGCTTACAGAGAG 300
Qy 946 TGGCTAGTCTGAAGTGTGCGACAGCTCAATCAGGCTGGAAATAAATAGAGCCGAT 1005
Db 301 TGGCTAGTCTGAAGTGTGCGACAGCTCAATCAGGCTGGAAATAAATAGAGCCGAT 360
Qy 1006 GTGGATGTTCTGAG 1019
Db 361 GTGGATGTTCTGAG 374

RESULT 10
AW125078/c
LOCUS AW125078 336 bp mRNA linear EST 22-OCT-1999
DEFINITION UI-M-BH2.1-apx-e-07-0-UI.s1 NIH BMAP_M.S3.1 Mus musculus cDNA clone
UI-M-BH2.1-apx-e-07-0-UI 3', mRNA sequence.
ACCESSION AW125078
VERSION AW125078.1 GI:6100608
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized prefrontal cortex library cDNA Library Preparation: M.B.

whole body"

Query Match 31.0%; Score 320.8; DB 1; Length 326;
 Best Local Similarity 99.4%; Pred. No. 4.1;
 Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 239 AGAGCTGGCTGGTGGCGGACCTACGCTCTTGGGCTGACCGCTCTGGATCCCGCCAGTCT 298
 Db 326 AGAAGCTGGCTGGTGGCGGACCTACGCTCTTGGGCTGACCGCTCTGGATCCCGCCAGTCT 267

Qy 299 GCGCGCTGTACCGAGTTTTCAGTCCCTGAGCTTGGTGGCTGGCCACAGTTGGGCTTT 358
 Db 266 GCGCGCTGTACCGAGTTTTCAGTCCCTGAGCTTGGTGGCTGGCCACAGTTGGGCTTT 207

Qy 359 CGCTATACAGCGCACCAACCGTGTGCCCGGGAAGTCAACAGAGCGGAGGAGC 418
 Db 206 CGCTATACAGCGCACCAACCGTGTGCCCGGGAAGTCAACAGAGCGGAGGAGC 147

Qy 419 GGTCCCGAGTGGTCCCAAGCCCTACTGGTTGAACCTTATCTGCGCATCGAGCAGTTCCG 478
 Db 146 GGTCCCGAGTGGTCCCAAGCCCTACTGGTTGAACCTTATCTGCGCATCGAGCAGTTCCG 87

Qy 479 AATTCGCCGAGCGCTCTGGTGGCGGAGCGGCGGAGCGGCTTTATAGCCACCTCTTAGA 538
 Db 86 AATTCGCCGAGCGCTCTGGTGGCGGAGCGGCGGAGCGGCTTTATAGCCACCTCTTAGA 27

Qy 539 TCAGCTCTATGAACAAACGTGCT 562
 Db 26 TCAGCTCTATGAACAAACGTGCT 3

RESULT 13
 CL631771
 LOCUS
 DEFINITION CMHD-GT 115G7-3 GTL R1 Gep-SD5 Mus musculus cDNA clone

CMHD-GT 115G7-3 3', mRNA sequence.
 CL631771
 CL631771.1 GI:49359294
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 255)
 Stanford, W.L.
 www.cmhd.ca
 Unpublished (2002)
 Contact: Stanford WL
 Institute of Biomaterials & Biomedical Engineering
 University of Toronto
 407 Rosebrugh Bldg., 4 Taddle Creek Rd., Toronto, Ontario, Canada
 M5S 3G9
 Tel: 416 946 8379
 Fax: 416 978 4317
 Email: william.stanford@utoronto.ca

Gep-SD5 Gene trap insertion. The sequence tag is generated by 3' race. The ES cell line harboring this insertion of the target gene is available through the following web site:
 http://pokey.ibe.utoronto.ca/sequence_report.php?id=115G7.
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 /strain="129S3"
 /db_xref="taxon:10090"
 /clone="CMHD-GT-115G7-3"
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 /cell_line="R1"
 /clone_lib="GTL R1 Gep-SD5"
 /note="Vector: Gep-SD5"

FEATURES
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 Best Local Similarity 99.4%; Pred. No. 4.1;
 Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Best Local Similarity 99.6%; Pred. No. 9.7;
 Matches 254; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 763 TGCATCTCTGCAGACTCTGTGCGGACTAGTATCCAGAGAGGGTGTACACAGGCTGG 822
 Db 1 TGCATCTCTGCAGACTCTGTGCGGACTAGTATCCAGAGAGGGTGTACACAGGCTGG 60

Qy 823 CCATTGATGTCTCCACCTGCCCAAGGACTGAAGGACTTCTGCAAGTACGAATGAACGA 882
 Db 61 CCATTGATGTCTCCACCTGCCCAAGGACTGAAGGACTTCTGCAAGTACGAATGAACGA 120

Qy 883 ATGAACGCTGTCTGTGGCCACCCAGAGCAAAAGTCCCGGTGGTGGCCCTCTTAGAG 942
 Db 121 ATGAACGCTGTCTGTGGCCACCCAGAGCAAAAGTCCCGGTGGTGGCCCTCTTAGAG 180

Qy 943 AAGTGGCTAGTCTGAGAGCTGGTGGCAGCTCAATCAGGGCTGGAAATAAATAGAGCC 1002
 Db 181 AAGTGGCTAGTCTGAGAGCTGGTGGCAGCTCAATCAGGGCTGGAAATAAATAGAGCC 240

Qy 1003 GATGTGATGTCTG 1017
 Db 241 GATGTGATGTCTG 255

RESULT 14
 CG487097
 LOCUS
 DEFINITION OST22480 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST22480,
 mRNA sequence.
 CG487097
 CG487097.1 GI:37245706
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 257)
 Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Piggott, J., Beltrandeirio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
 Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 14610273
 Contact: Zambrowicz BP
 OmniBank

Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
 1..257
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 Best Local Similarity 99.2%; Pred. No. 10;
 Matches 251; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 4 CCTCTCTGCAGACTCTGTGGCGACTAGTGATCCAGAGAGGGTGGTACACAGGCTGGCCA 63
QY 826 TTGATGTGCTCCACTGCCCAAGGACTGAAGGACTTCTGCAAGTACGAATGAACGAATG 885
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QY 886 AACGCTGTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTGCTCTAGAGAAG 945
Db 124 AACGCTGTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTGCTCTAGAGAAG 183
QY 946 TGGCTAGTCTGAAGCTGTGGCCACAGCTCAAAATCAGGCGTGGAAATAAATAGAGCCGAT 1005
Db 184 TGGCTAGTCTGAAGCTGTGGCCACAGCTCAAAATCAGGCGTGGAAATAAATAGAGCCGAT 243
QY 1006 GTGGATGTTCTGA 1018
Db 244 GTGGATGTTCTGA 256

RESULT 15
CG479214 251 bp mRNA linear GSS 01-OCT-2003
LOCUS OST9837 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST9837, mRNA
DEFINITION sequence.
ACCESSION CG479214
VERSION CG479214.1 GI:37230103
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 251)
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Spark, M.J., Van Slichtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
COMMENT Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source
location/Qualifiers
1..251
/organism="Mus musculus"
/mol_type="mRNA"
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/clone="OST9837"
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Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 766 CATCTCTGCAGACTCTGTGGCGACTAGTGATCCAGAGAGGGTGGTACACAGGCTGGCCA 825
Db 5 CCTCTCTGCAGACTCTGTGGCGACTAGTGATCCAGAGAGGGTGGTACACAGGCTGGCCA 64
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Db 125 AACGCTGTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCCCTGCTCTAGAGAAG 184
QY 946 TGGCTAGTCTGAAGCTGTGGCCACAGCTCAAAATCAGGCGTGGAAATAAATAGAGCCGAT 1005
Db 185 TGGCTAGTCTGAAGCTGTGGCCACAGCTCAAAATCAGGCGTGGAAATAAATAGAGCCGAT 244
QY 1006 GTGGATG 1012
Db 245 GTGGATG 251

RESULT 16
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LOCUS BX632311 pBluescript Lion Mus musculus cDNA clone LIONp462C0276 3',
DEFINITION mRNA sequence.
ACCESSION BX632311
VERSION BX632311.1 GI:33612186
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 228)
AUTHORS Henrich, J., Hermanns, J., Kranz, H., Loeblert, R., Schluter, T.,
Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Mouse ArrayTAG cDNA (LION)
Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; LIONp462C0276.
RZPDLIB;
Mouse ArrayTAG cDNA (LION)
http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=4
62 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACAGCTATGAC.
FEATURES
source
location/Qualifiers
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Db 228 GACTAGTATCCAGAGAGGGTGGTACACAGGCTGGCCATTGATGTGCTCACCTGCCCA 169
QY 847 AAGGACTGAAGGACTTCTGCAAGTACGAATGAACGCTGTCTGTGCGCCACCA 906
Db 168 AAGGACTGAAGGACTTCTGCAAGTACGAATGAACGCTGTCTGTGCGCCACCA 109
QY 907 GAGCAAAAGTCCCGGTGGTGGCCCTGCTCTAGAGAAGTGGCTAGTCTGAAGCTGCTCG 966

```

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108 GAGCAAGTCCCGTGGTGGCCCTGCTCTAGAGAGTGGCTAGTCTGAAGCTGGTGG 49
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QY 967 CACAGCTCACATCAGGCTGGAATAAATAGAGCCGATGGGA 1010
|||||
Db 48 CACAGCTCACATCAGGCTGGAATAAATAGAGCCGATGGGA 5
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RESULT 17
CX214893/c
LOCUS
DEFINITION MNS23392 Mouse Neurosphere Normalized cDNA library Mus musculus
          200 bp mRNA linear EST 29-DEC-2004
          cDNA 5', mRNA sequence.
ACCESSION CX214893
VERSION CX214893.1 GI:56870185
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 200)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus..
AUTHORS Williams, C., Wirta, V., Lundberg, J. and Frisen, J.
TITLE Expressed sequence tags of cDNA clones from murine neurospheres
JOURNAL Unpublished (2005)
COMMENT Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
Albano University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel.: +46855378332
Fax: +46855378481
Email: cecilia.williams@biotech.kth.se
Seq primer: M13REV.
Location/Qualifiers
1..200
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/sex="MALE"
/tissue_type="Lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"
/dev_stage="Adult"
/clone_lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVSPORT6.0; A cDNA
library was constructed in pCMVSPORT6.0 from RNA isolated
from neurospheres of adult male and female mice. Custom
normalized cDNA library by Invitrogen/ResGen"

Query Match 19.2%; Score 199; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 CCGTGTGCCCCGGGAGGTCAACAGAGCGGAGCGGTCGCCAGTGGTCCCAAGC 439
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QY 440 CTTACTGTGTGAACCTATCTGCGATCGAGCAGTTCGGAATTCGCCGGACCGTCTGT 499
Db 139 CTTACTGTGTGAACCTATCTGCGATCGAGCAGTTCGGAATTCGCCGGACCGTCTGT 80
QY 500 GGGCCGACGCGCGCAGGCGTTTATAGCCACCTCTTAGATCAGCTCTATGAACAAAGCT 559
Db 79 GGGCCGACGCGCGCAGGCGTTTATAGCCACCTCTTAGATCAGCTCTATGAACAAAGCT 20
QY 560 GTGCTCTCTACAGCGGC 578
Db 19 GTGCTCTCTACAGCGGC 1
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RESULT 18
AV022299

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LOCUS
DEFINITION AV022299 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
          clone 1190026D24, mRNA sequence.
ACCESSION AV022299
VERSION AV022299.1 GI:4799291
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 195)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus..
AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsuma, H., Oda, H.,
Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
Suganara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y.,
Tomihata, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T.,
Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
Location/Qualifiers
1..195
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1190026D24"
/sex="mixed"
/dev_stage="18-day embryo"
/clone_lib="Mus musculus 18-day embryo C57BL/6J"

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Best Local Similarity 97.9%; Pred. No. 22;
Matches 191; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 823 CCATTGATGCTCCACCTGCGCCCAAGGACCTGAGGACTCTCTGCAAGTACGAATGAACGA 882
Db 1 CCATTGATGCTCCACCTGCGCCCAAGGACCTGAGGACTCTCTGCAAGTACGAATGAACGA 60
QY 883 ATGAACGCTCTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCGCTCTGCTCTAGAG 942
Db 61 ATGAACGCTCTCTGTGGCCACAGAGCAAAAGTCCCGGTGGTGGCGCTCTGCTCTAGAG 120
QY 943 AAGTGGCTAGTCTGAAGCTGTGTCAGCAGCTCACAATCAGGGCTGGAATAAATAGAGCC 1002
Db 121 AAGTGGCTAGTCTGAAGCTGTGTCAGCAGCTCACAATCAGGGCTGGAATAAATAGAGCC 180
QY 1003 GATGGGATGTTCTG 1017
Db 181 GATGGGATGTTTGG 195
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Search completed: March 2, 2006, 10:53:14
Job time : 5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:54:58 ; Search time 1 Seconds
(without alignments)
3.181 Million cell updates/sec

Title: US-10-014-774-1
Perfect score: 1036
Sequence: 1 cccgtgtgcagcgttgagg.....gagaaaaa.....gagaaaaa 1036

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 1535 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 10
Maximum DB seq length: 1036

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : us-10-014-774-1.sl.rng4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1036	100.0	1036	1 AAA89043	Murine muscle-spec
2	487.5	47.1	499	1 AAA89047	Mouse muscle-speci

ALIGNMENTS

RESULT 1
AAA89043
ID AAA89043 standard; cDNA; 1036 BP.
XX AC AAA89043;
XX
XX 05-MAR-2001 (first entry)
XX DE Murine muscle-specific protein Ozz cDNA.
XX
XX Ozz; mouse; muscle-specific protein; myogenesis; muscle damage;
KW galactosialidosis; myocardial infarction; angina; therapy; diagnosis; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX 21..878
XX CDS /*tag= a
XX
XX WO20006733-A1.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011900.
XX
XX 29-APR-1999; 99US-013181P.
PR

XX (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
PA D'azzo A, Bongiovanni A, Nastasi T;
XX
XX WPI; 2001-007221/01.
DR P-PSDB; AAB19850.
XX Novel protein Ozz and nucleic acid encoding the protein involved in
XX development and function of muscle, useful as target for identifying
XX drugs effective in treating myogenesis disorders.
XX Claim 6; Fig 2A; 62pp; English.
XX
XX The present sequence is that of cDNA encoding a novel murine muscle-
XX specific protein, termed Ozz (see AAB19850), that regulates development
XX and function of muscle cells. The Ozz gene was identified overlapping
XX exon 1a of the murine PPCA gene, transcribed on the opposite strand. The
XX corresponding cDNA was isolated from a mouse heart library. It shows 85%
XX homology to human Ozz cDNA (see AAB9044). The murine Ozz protein is
XX preferentially expressed by a 1.0 kb mRNA in heart and skeletal muscle.
XX This protein shares homology with neuralised proteins, associated with a
XX number of muscle proteins, including beta-catenin. Ozz protein is useful
XX for detecting damage to muscle tissue or disease associated with a defect
XX in Ozz expression. Increase in the level of Ozz protein in blood or in a
XX blood fraction indicates damage to muscle tissue in the heart and an
XX abnormal level or localization of Ozz in muscle cells from the atrium of
XX the heart of a subject is useful for detecting galactosialidosis
XX (claimed). The presence of Ozz in blood or a blood fraction indicates
XX muscle tissue damage e.g. ischaemia associated with either unstable
XX angina, myocardial infarction or both. Nucleotide sequences derived from
XX the gene encoding Ozz and peptide sequences derived from Ozz are useful
XX as targets to identify drugs that are effective in treating myogenesis
XX disorders
XX
XX Sequence 1036 BP; 215 A; 321 C; 297 G; 203 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1036;	DB 1;	Length 1036;
Best Local Similarity	100.0%;	Pred. No. 0;		
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QY 61	GGAGCCCTGCGCGCCAGAGCCCTCCACCCGCTTCCACCAAGTCATGGAGCAACA	120		
DB 61	GGAGCCCTGCGCGCCAGAGCCCTCCACCCGCTTCCACCAAGTCATGGAGCAACA	120		
QY 121	TCCGCATGAGCCCTCAGGAACCGGAGCCACACCGCTGGAGAGTTTCGCCACCGTGTGT	180		
DB 121	TCCGCATGAGCCCTCAGGAACCGGAGCCACACCGCTGGAGAGTTTCGCCACCGTGTGT	180		
QY 181	GCTTCAGTCGTGAGCCCTCGGCCCGCCAGGATATTTCTAGTGAATTTGAGGAAAAG	240		
DB 181	GCTTCAGTCGTGAGCCCTCGGCCCGCCAGGATATTTCTAGTGAATTTGAGGAAAAG	240		
QY 241	AGCTGGCTGTGTGGGGGACCTTACGCTTGGCTGACCGCTGATGATCCCGCAGTCTGG	300		
DB 241	AGCTGGCTGTGTGGGGGACCTTACGCTTGGCTGACCGCTGATGATCCCGCAGTCTGG	300		
QY 301	CCGCTGTATCCCGAGTTTTTCACTGCTGAGCTTGGTTCAGCTTGGCCACAGTTGGGTCTTCG	360		
DB 301	CCGCTGTATCCCGAGTTTTTCACTGCTGAGCTTGGTTCAGCTTGGCCACAGTTGGGTCTTCG	360		
QY 361	CTATCACAGCCACCAACCCGTGTGTCGCCGGAAGGTCAACACAGAGCGGAGCGGG	420		
DB 361	CTATCACAGCCACCAACCCGTGTGTCGCCGGAAGGTCAACACAGAGCGGAGCGGG	420		
QY 421	TCCCGAGTGTGTCGCCGAGCCCTTACTGCTTGAACCTTATCTGCGCATCGAGCAATCCGAA	480		
DB 421	TCCCGAGTGTGTCGCCGAGCCCTTACTGCTTGAACCTTATCTGCGCATCGAGCAATCCGAA	480		

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Job time : 1 secs

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Sequence 14: Appl

ALIGNMENTS

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US-10-014-774-1
; Sequence 1, Application US10014774
; Publication No. US20020099173A1
; GENERAL INFORMATION:
; APPLICANT: D'Azzo, Alessandra
; APPLICANT: Bongiovanni, Antonella
; APPLICANT: Nastasi, Tommaso
; TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle
; FILE REFERENCE: 2427/1F509-US1
; CURRENT APPLICATION NUMBER: US/10/014, 774

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, CURRENT FILING DATE: 2001-10-29
 , PRIOR APPLICATION NUMBER: PCT/US00/11900
 , PRIOR FILING DATE: 2000-04-28
 , PRIOR APPLICATION NUMBER: US 60/131.814
 , PRIOR FILING DATE: 1999-04-29
 , NUMBER OF SEQ ID NOS: 24
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Total number of hits satisfying chosen parameters: 66

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1

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; LENGTH: 1036

; TYPE: DNA

; ORGANISM: M

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Matches 1036;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

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QY	1	CCCTGTTGACAGCGCTTGGAGATCGCTCTCCCTCCGAACACGTAGGACTGGTGTCGCCAC	60
Db	1	CCCTGTTGACAGCGCTTGGAGATCGCTCTCCCTCCGAAACACGTAGGACTGGTGTCGCCAC	60
QY	61	GGAGCCCTCGCGCCCGCAGAGCCCCCTCCACCCGCTTCCACCAAGTCATGAGGCCAACA	120
Db	61	GGAGCCCTCGCGCCCGCAGAGCCCCCTCCACCCGCTTCCACCAAGTCATGAGGCCAACA	120
QY	121	TCGCGCATGAGACCCCTCAGGAAACGGAGCCACAACGCTGGAGAGTTTCGCCACACGGTGTGT	180
Db	121	TCGCGCATGAGACCCCTCAGGAAACGGAGCCACAACGCTGGAGAGTTTCGCCACACGGTGTGT	180
QY	181	GCTTTCAGTCGTGAGCCCCCTGGCCCCCGGCCAGGTATTTCTAGTCGAAATTCAGGAAAAAG	240
Db	181	GCTTTCAGTCGTGAGCCCCCTGGCCCCCGGCCAGGTATTTCTAGTCGAAATTCAGGAAAAAG	240
QY	241	AGCTGGGCTGGTCGGGSCACTAGCTCTTGGCCCTGACCGCTCTCGATCCGCCCACTCTGG	300
Db	241	AGCTGGGCTGGTCGGGSCACTAGCTCTTGGCCCTGACCGCTCTCGATCCGCCCACTCTGG	300
QY	301	CCGCTGTACCCGAGTTTTTCACTGCTCAGCTTGGTCAGCCTTGGCCACAGTTGGGTCTTCG	360
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QY	361	CTATCACAGCCACCAACACCGTGTGCCCGGGAAGGTCAACAGAGCGGAGGCGGCGG	420
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QY	421	TCGCCAGTGTGCCAAGCCCTACTGTTGAAACCTATCTCGGCATCGAGCAGTTCGAA	480
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QY	481	TTCCCGGGGACCGTCTGGTGGGCGCAGCGGCCAGGGCTTTATAGCCACCTCTTAGATC	540
Db	481	TTCCCGGGGACCGTCTGGTGGGCGCAGCGGCCAGGGCTTTATAGCCACCTCTTAGATC	540
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Db 661 GCGCTAGCGCCCGGGGCTGCGAGCTGCTCAGCCCTCTAGCTGTGGTAGATGTGTTG 720
Qy 721 CTTCCACAAGAGCGTGTGCTGTGTCAGCTGGAGTAGTGGCTGCCATCTCTGAGACTC 780
Db 721 CTTCCACAAGAGCGTGTGCTGTGTCAGCTGGAGTAGTGGCTGCCATCTCTGAGACTC 780
Qy 781 TGTGCCAGTACTGATCCAGAAAGGGTGTGACACAGGCTGGCCATTGATGTGTCACC 840
Db 781 TGTGCCAGTACTGATCCAGAAAGGGTGTGACACAGGCTGGCCATTGATGTGTCACC 840
Qy 841 TGCCCAAGGACTCAAGGACTTCTGCAAGTACGAATGAACGAATGAACGCTGTCTGTGG 900
Db 841 TGCCCAAGGACTCAAGGACTTCTGCAAGTACGAATGAACGAATGAACGCTGTCTGTGG 900
Qy 901 CCACGAGCAAGTCCCCGGTGTGCGCCCTGCTCTAGAGAGTGGCTAGTCTGAAGC 960
Db 901 CCACGAGCAAGTCCCCGGTGTGCGCCCTGCTCTAGAGAGTGGCTAGTCTGAAGC 960
Qy 961 TGGTGGCACAGCTCACATCAGGCTGGAATAATAATAGAGCCGATGTGGATGTTCTGAGA 1020
Db 961 TGGTGGCACAGCTCACATCAGGCTGGAATAATAATAGAGCCGATGTGGATGTTCTGAGA 1020
Qy 1021 AAAAAAAAAAAAAA 1036
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; Sequence 14, Application US/10014774
; Publication No. US20020099173A1
; GENERAL INFORMATION:
; APPLICANT: D'Azzo, Alessandra
; APPLICANT: Bongiovanni, Antonella
; APPLICANT: Nastasi, Tommaso
; TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle
; FILE REFERENCE: 2427/1F509-US1
; CURRENT APPLICATION NUMBER: US/10/014, 774
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/US00/11900
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,814
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-014-774-14
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Best Local Similarity 99.8%; Pred. No. 1.9e-05;
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Qy 265 GTCTTGGCTGACCGCTCTGGATCCCGCAGTCTGGCGGCTGTATCCGAGTTTCACTGC 324
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Qy 325 CTGACTTGGCTGACCGCTTGGCCACAGTTGGTCTTGGCTATCACAGCCACCAACCGTG 384
Db 439 CTGACTTGGCTGACCGCTTGGCCACAGTTGGTCTTGGCTATCACAGCCACCAACCGTG 380
Qy 385 TGCCCGGGAGGTCACAGCAAGCGGAGGCGGCTCCCGAGTGGTCCCCCAAGCCCTAC 444
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Db 379 TGCCCGGGAAAGGTCAACCAAGAGCGAGCGGTCCCGAGTGTGTCCTCCCAAGCCCTAC 320
Qy 445 TGCTTGAACCCCTATCTCGGCATCGAGCAGTTCGGAATTCCTCCGGGACCGTCTGTTGGCC 504
Db 319 TGCTTGAACCCCTATCTCGGCATCGAGCAGTTCGGAATTCCTCCGGGACCGTCTGTTGGCC 260
Qy 505 GCAGCGCGCCAGGGCTTTATAGCCACTCTTAGATCAGCTCTATGAACAAAAAGTGTGTC 564
Db 259 GCAGCGCGCCAGGGCTTTATAGCCACTCTTAGATCAGCTCTATGAACAAAAAGTGTGTC 200
Qy 565 CTCTACAGCGCCGAGCGCTTGGGTGTTCTTCTTGTGCCCCCTGAGGATGGGACCG 624
Db 199 CTCTACAGCGCGCCGAGCGCTTGGGTGTTCTTCTTGTGCCCCCTGAGGATGGGACCG 140
Qy 625 CCACATGACATCATCATCAACGGGGAGGACATGGGCCCCCTAGCGCCCCGGGGCTGCCAG 684
Db 139 CCACATGACATCATCATCAACGGGGAGGACATGGGCCCCCTAGCGCCCCGGGGCTGCCAG 80
Qy 685 CTCTCAGCGCCCTCTACGCTGTGGTAGATGTGTTGTTCTTCCACCAAGAGCGT-CCGTCTG 743
Db 79 CTCTCAGCGCCCTCTACGCTGTGGTAGATGTGTTGTTCTTCCACCAAGAGCGTGTGCGCTG 20
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RESULT 3
US-10-719-900-53916
; Sequence 53916, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719, 900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427, 808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 53916
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-53916
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Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 581 AAGCCGCTGGGTGTTCTTCTTCTGC 605
Db 1 AAGCCGCTGGGTGTTCTTCTTCTGC 25
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RESULT 4
US-10-719-900-162890
; Sequence 162890, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719, 900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427, 808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 162890
; LENGTH: 25
; TYPE: DNA
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```

; ORGANISM: Mus musculus
US-10-719-900-162890

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 710 AGATGCTTTGCTTCCACCAAGAGC 734
Db 1 AGATGCTTTGCTTCCACCAAGAGC 25

RESULT 5
US-10-719-900-266177
; Sequence 266177, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 266177
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-266177

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 616 ATGGGACCGCGGACATGCACATCAT 640
Db 1 ATGGGACCGCGGACATGCACATCAT 25

RESULT 6
US-10-719-900-297068
; Sequence 297068, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 297068
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-297068

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 728 CAAGAGCGTGCTCTGCTCCAGCTG 752
Db 1 CAAGAGCGTGCTCTGCTCCAGCTG 25

RESULT 7
US-10-719-900-685399
; Sequence 685399, Application US/10719900

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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 685399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-685399

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 744 GTCCAGCTGGAGTATGCTTGCCAT 768
Db 1 GTCCAGCTGGAGTATGCTTGCCAT 25

RESULT 8
US-10-719-900-705299
; Sequence 705299, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 705299
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-705299

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 924 GTGCGCCCTGCTCTAGAGAGTGG 948
Db 1 GTGCGCCCTGCTCTAGAGAGTGG 25

RESULT 9
US-10-719-900-843156
; Sequence 843156, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 843156
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

```

US-10-719-900-843156

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 876 TGAACGAATCAAGCCCTGCTGTGG 900
|||||
Db 1 TGAACGAATCAAGCCCTGCTGTGG 25

RESULT 10

US-10-719-900-870471
; Sequence 870471, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 870471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-870471

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 TGGCATCGAGCAGTTCGGAATCC 484
|||||
Db 1 TGGCATCGAGCAGTTCGGAATCC 25

RESULT 11

US-10-719-900-886835
; Sequence 886835, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 886835
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-886835

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 946 TGGTAGTCTGAAGCTGGTCGACA 970
|||||
Db 1 TGGTAGTCTGAAGCTGGTCGACA 25

RESULT 12

US-10-719-900-894080
; Sequence 894080, Application US/10719900
; Publication No. US20050026164A1

GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 894080
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-894080

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 961 TGGTCGACAGCTCACAATCAGGC 985
|||||
Db 1 TGGTCGACAGCTCACAATCAGGC 25

RESULT 13

US-10-719-900-896569
; Sequence 896569, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 896569
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-896569

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 445 TGGTTGAACCTATCTGCCATCGA 469
|||||
Db 1 TGGTTGAACCTATCTGCCATCGA 25

RESULT 14

US-11-036-317-85479/c
; Sequence 85479, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 85479
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-11-036-317-85479

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 AGCCCTACTGGTTGAACCCCTATCTG 461
Db 25 AGCCCTACTGGTTGAACCCCTATCTG 1

RESULT 15

US-11-036-317-99886/c
; Sequence 99886, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 99886
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-99886

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 CAGCCTTGGCCACAGTTGGGCTTC 359
Db 25 CAGCCTTGGCCACAGTTGGGCTTC 1

RESULT 16

US-11-036-317-117157/c
; Sequence 117157, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 117157
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-117157

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 TCGCATCGAGCAGTTCGGAATTC 484
Db 25 TCGCATCGAGCAGTTCGGAATTC 1

RESULT 17

US-11-036-317-118199/c

; Sequence 118199, Application US/11036317
; Publication No. US20050214823A1

; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118199
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-11-036-317-118199

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 265 GTCTTGGCTGACGGCTCTGGATCC 289
Db 25 GTCTTGGCTGACGGCTCTGGATCC 1

RESULT 18

US-11-036-317-121303/c
; Sequence 121303, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121303
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-121303

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 507 AGCCGGCCAGGGCTTTATAGCCACC 531
Db 25 AGCCGGCCAGGGCTTTATAGCCACC 1

RESULT 19

US-11-036-317-122357/c
; Sequence 122357, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 122357
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-122357

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 CTGCGCGCTGTACCGAGTTTTCAC 321
|||||
Db 25 CTGCGCGCTGTACCGAGTTTTCAC 1

RESULT 20

US-11-036-317-124848/c
; Sequence 124848, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 124848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-124848

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 GCCAGGGCTTTATAGCCACCTCTTA 536
|||||
Db 25 GCCAGGGCTTTATAGCCACCTCTTA 1

RESULT 21

US-11-036-317-137071/c
; Sequence 137071, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 137071
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-137071

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CCCGGGAAGGTCACCAAGAGCGGA 412
|||||
Db 25 CCCGGGAAGGTCACCAAGAGCGGA 1

RESULT 22

US-11-036-317-138129/c
; Sequence 138129, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 138129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-138129

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 TGGTTGAACCTTATCTGCGCATCGA 469
|||||
Db 25 TGGTTGAACCTTATCTGCGCATCGA 1

RESULT 23

US-11-036-317-148396/c
; Sequence 148396, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 148396
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-148396

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 GTTGGGTCTTCGCTATCACAGCCA 373
|||||
Db 25 GTTGGGTCTTCGCTATCACAGCCA 1

RESULT 24

US-11-036-317-565796/c
; Sequence 565796, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13

;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 565796
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-565796

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 AGCCCTACTGTTGAACCTATCTG 461
Db 25 AGCCCTACTGTTGAACCTATCTG 1

RESULT 25
US-11-036-317-632291/c
; Sequence 632291, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 632291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-632291

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 CAGCCTTGCCACAGTTGGTCTTC 359
Db 25 CAGCCTTGCCACAGTTGGTCTTC 1

RESULT 26
US-11-036-317-699875/c
; Sequence 699875, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 699875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-699875

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 TGGCATCGAGCAGTTCGGAATCC 484
Db 25 TGGCATCGAGCAGTTCGGAATCC 1

RESULT 27
US-11-036-317-704471/c
; Sequence 704471, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 704471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-704471

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 265 GTCTTGGCCTGACCGCTCTGGATCC 289
Db 25 GTCTTGGCCTGACCGCTCTGGATCC 1

RESULT 28
US-11-036-317-720585/c
; Sequence 720585, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 720585
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-720585

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 507 AGCCGGCCAGGCTTTATAGCCACC 531
Db 25 AGCCGGCCAGGCTTTATAGCCACC 1

RESULT 29
US-11-036-317-726995/c
; Sequence 726995, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John

```
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 726995
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-726995

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 CTGCCGCTGTACCGAGTTTTCAC 321
      |||||||
Db 25 CTGCCGCTGTACCGAGTTTTCAC 1

RESULT 30
US-11-036-317-737834/c
; Sequence 737834, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 737834
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-737834

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 GCCAGGGCTTTATAGCCACCTCTTA 536
      |||||||
Db 25 GCCAGGGCTTTATAGCCACCTCTTA 1

RESULT 31
US-11-036-317-775667/c
; Sequence 775667, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 775667
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-775667
```

```
Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CCGGGAAGGTCAACCAAGAGCGGA 412
      |||||||
Db 25 CCGGGAAGGTCAACCAAGAGCGGA 1

RESULT 32
US-11-036-317-780021/c
; Sequence 780021, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 780021
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-780021

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 TGGTTGAACCCCTATCTGCGCATCGA 469
      |||||||
Db 25 TGGTTGAACCCCTATCTGCGCATCGA 1

RESULT 33
US-11-036-317-819409/c
; Sequence 819409, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 819409
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-819409

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 45;
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QY 349 GTTGGGTCTTCGCTATCACACGCCA 373
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Db 25 GTTGGGTCTTCGCTATCACACGCCA 1

RESULT 34
US-10-014-774-1/c
; Sequence 1, Application US/10014774
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; Publication No. US20020099173A1
; GENERAL INFORMATION:
; APPLICANT: D'Azzo, Alessandra
; APPLICANT: Bongiovanni, Antonella
; APPLICANT: Nastasi, Tommaso
; TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle
; FILE REFERENCE: 2427/1F509-US1
; CURRENT APPLICATION NUMBER: US/10/014,774
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/US00/11900
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,814
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-014-774-1

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Best Local Similarity 51.0%; Pred. No. 1.2;
Matches 52; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 221 AGTGGAAATTCAGGAAAGAGCTGGCTGGTGGCGGCACCTAGCTCTTGGCCCTGACCGC 280
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Qy 281 TCTGATCCCCCAGCTCTGGCGCTGTACCCGAGTTTCACT 322
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RESULT 35
US-10-014-774-14
; Sequence 14, Application US/10014774
; Publication No. US20020099173A1
; GENERAL INFORMATION:
; APPLICANT: D'Azzo, Alessandra
; APPLICANT: Bongiovanni, Antonella
; APPLICANT: Nastasi, Tommaso
; TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle
; FILE REFERENCE: 2427/1F509-US1
; CURRENT APPLICATION NUMBER: US/10/014,774
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/US00/11900
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,814
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; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
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; SOFTWARE: PatentIn version 3.3
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; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-916337

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; Sequence 1020143, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
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; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1020143

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 CTCGAGAAAAA 1

RESULT 6

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; Sequence 589295, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 589295
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-589295

Query Match 2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: March 2, 2006, 10:57:51
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DEFINITION Homo sapiens neuralized-like 2 (Drosophila), mRNA (cDNA clone
MGC:103813 IMAGE:30915194), complete cds.
ACCESSION BC074737
VERSION BC074737.2 GI:50960526
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, J., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Hsieh, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
Schnerker, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 916)
AUTHORS Director MGC Project.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NTH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT On Aug 4, 2004 this sequence version replaced gi:49902602.
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
Centre
cDNA Library Preparation: British Columbia Cancer Research Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Anara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angélique Schnerch, Ursula Skalska,
Duane Smalish, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Qy	260	CTGCGTCTCGGTGACACCGCTGAGACCCCGCAGTCTGGCCCCCGTTCCCGAGTTTCT	319
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Qy	320	CTGCGCGATCTGGTCAACTGGGCCACACTGGGTCTTCGCCATCAACGCCACACACAC	379
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:21:36 ; Search time 2 Seconds
(without alignments)
3.520 Million cell updates/sec

Title: US-10-014-774-3

Perfect score: 970

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 5 seqs, 3629 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0

Maximum DB seq length: 970

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 5 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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VERSION DQ049741.1 GI:66902940
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Hominidae; Homo.
1 (bases 1 to 858)
Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)
PUBLISHED 15869325
REFERENCE 2 (bases 1 to 858)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Gnanowski, S., Sackton, T.B.,

Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES

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Matches 858; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 726; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 728 CCTGCCCTATGGCGGAGAGATGGTGTGCTCGAGCCGCTGATTCGGGTGCACCTCTG 669
Qy 61 GGGACTCGAGCGCCCGGAGCCGCC - TCCACCCCGCTTCCATCGGGTGCACGGTGCCAAACA 119
Db 668 GGGACTCGAGCGCCCGGAGCCGCC - TCCACCCCGCTTCCATCGGGTGCACGGTGCCAAACA 609
Qy 120 TCGCGTGGACCCCTCTGGAGCGGGGCCACACGCTGGAGAGCTTGCCTCCACGGCGTGT 179
Db 608 TCGCGTGGACCCCTCTGGAGCGGGGCCACACGCTGGAGAGCTTGCCTCCACGGCGTGT 549
Qy 180 GCTTCAGCGCGGAGCGCTGCGCCCGGCGGAGGCTTCTCGTGTGAGATCGAGGAGAAAG 239
Db 548 GCTTCAGCGCGGAGCGCTGCGCCCGGCGGAGGCTTCTCGTGTGAGATCGAGGAGAAAG 489
Qy 240 AGCTGGGCTGGTGGGACATCTGCGTCTCGGTCTGACCGGCTGAGCCCGCCAGTCTGG 299
Db 488 AGCTGGGCTGGTGGGACATCTGCGTCTGACCGGCTGAGCCCGCCAGTCTGG 429
Qy 300 CCCCCTGTCCCGAGTTTCTGTGCCGATCTGTGTCACCTGGGGCCACACCTGGGCTTTCG 359
Db 428 CCCCCTGTCCCGAGTTTCTGTGCCGATCTGTGTCACCTGGGGCCACACCTGGGCTTTCG 369
Qy 360 CCATCAGCGCGCACCAACCGCGTGGCCGGGAGGGCGCCCGGAGGCGGAGGACGCGG 419
Db 368 CCATCAGCGCGCACCAACCGCGTGGCCGGGAGGGCGCCCGGAGGCGGAGGACGCGG 309
Qy 420 CCCCAGCGGACCTTCCAAACCTCTCGTGGAAACATATCTCGCATTTGAGCAGTTTCGCA 479
Db 308 CCCCAGCGGACCTTCCAAACCTCTCGTGGAAACATATCTCGCATTTGAGCAGTTTCGCA 249
Qy 480 TTCCCGGAGCCGCTGTGTGGCGCGCAGCCGGCCAGGGCTCTA CAGCCATCTCTTGGACC 539
Db 248 TTCCCGGAGCCGCTGTGTGGCGCGCAGCCGGCCAGGGCTCTA CAGCCATCTCTTGGACC 189
Qy 540 AGCTCTATGAGCTGAACGTGTGCTCGACCGCGCGCGGTAGCGGCTGGGTCTCTCT 599
Db 188 AGCTCTATGAGCTGAACGTGTGCTCGACCGCGCGCGGTAGCGGCTGGGTCTCTCT 129
Qy 600 TTTCGCGCGCCCGATGSCAGCGGCACATGACATCATCATCAACGGCGAGACATGG 659
Db 128 TTTCGCGCGCCCGATGSCAGCGGCACATGACATCATCATCAACGGCGAGACATGG 69
Qy 660 GCGCGAGCGCCCGGGGAGTGGCAGCTGGCGAGCCCTCTACGCGGTGGTGGACGTTTGG 719
Db 68 GCGCGAGCGCCCGGGGAGTGGCAGCTGGCGAGCCCTCTACGCGGTGGTGGACGTTTGG 9
Qy 720 CTTCCACA 727
Db 8 CTTCCACA 1
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RESULT 4
AL844375 581 bp mRNA linear EST 30-JUL-2002
LOCUS AL844375 pool_AB_lib_v_SPB Homo sapiens cDNA, mRNA sequence.
DEFINITION AL844375
ACCESSION AL844375
VERSION AL844375.1 GI:22019153
KEYWORDS EST.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 581)
Ashcroft,K., Bethel,G., Bye,J.M., Howell,G.R., Huckle,E.J. and
Sheridan,E.
Homo sapiens EST sequence
Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : sccdl1472.1587085
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool AB lib v_SPB cDNA library. Further information can be found at
http://www.sanger.ac.uk/Teams/Team69/.

FEATURES
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source          1..581
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Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 298 GGGCCCCGTTCCGAGTTTCTGTGCCGATCTGTCAACCTGGGCCACACCTGGGCTT 357
Db 1 GGGCCCCGTTCCGAGTTTCTGTGCCGATCTGTCAACCTGGGCCACACCTGGGCTT 60
Qy 358 GCGCATCAGCGCCACCAACCGCGTGGCCGGAGGGCGCCCGGAGGCGGAGGAGC 417
Db 61 GCGCATCAGCGCCACCAACCGCGTGGCCGGAGGGCGCCCGGAGGCGGAGGAGC 120
Qy 418 GGGCCCCAGCGACCTCCAAACCTCTCGTGGAAACATATCTGCGCATTTGAGCAGTTTCG 477
Db 121 GGGCCCCAGCGACCTCCAAACCTCTCGTGGAAACATATCTGCGCATTTGAGCAGTTTCG 180
Qy 478 CATTTCCCGGAGCCGCTGTGTGGCGCGCAGCCGGCCAGGGCTCTACAGCCATCTCTTGGGA 537
Db 181 CATTTCCCGGAGCCGCTGTGTGGCGCGCAGCCGGCCAGGGCTCTACAGCCATCTCTTGGGA 240
Qy 538 CCAGCTCTATGAGCTGAACGTGTGCTCGACCGCGCGCGGTAGCGGCTGGGTCTCT 597
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Qy 598 CTTTTTCCCGCGCCCGATGSCAGCGGCACATGACATCATCATCAACGGCGAGGACAT 657
Db 301 CTTTTTCCCGCGCCCGATGSCAGCGGCACATGACATCATCATCAACGGCGAGGACAT 360
Qy 658 GGGCGCGAGCGCCCGGGGAGTGGCAGCTGGCGAGCCCTCTACGCGGTGGTGGACGTTT 717
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Qy 718 TGCTTCCACAAGAGCGTGGCGCTTGTCCAGCTCGAGTATGGCTTGCATCCCTGCCAGAC 777
Db 421 TGCTTCCACAAGAGCGTGGCGCTTGTCCAGCTCGAGTATGGCTTGCATCCCTGCCAGAC 480
Qy 778 TCTGTGCGGCTAGTATACAAAGAGCATGTCGTCACCGGCTGGCCATTGATGGCTCCA 837
Db 481 TCTGTGCGGCTAGTATACAAAGAGCATGTCGTCACCGGCTGGCCATTGATGGCTCCA 540
Qy 838 CTTGCCCAAGAACTTAAGGATTTCTGCAAGTATGAGTGAA 878
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Db 541 CCTGCCCAAGAACTTAAGGATTCTGAAGTATGAGTGAA 581

RESULT 5
AL844376/c
LOCUS
DEFINITION AL844376 pool_AB_lib_v_SPB Homo sapiens cDNA, mRNA linear EST 30-JUL-2002
ACCESSION AL844376
VERSION AL844376.1 GI:22019154
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 590)
Ashcroft,K., Bethel,G., Bye,J.M., Howell,G.R., Huckle,E.J. and
Sheridan,E.
Homo sapiens EST sequence
Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : scdd11472.400427A
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool_AB_lib_v_SPB cDNA library. Further information can be found at
<http://www.sanger.ac.uk/teams/Team69/>.
Location/Qualifiers
1..590
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/mol_type="mRNA"
/db_xref="taxon:9606"
/map="20"
/clone_lib="pool_AB_lib_v_SPB"

Query Match 59.2%; Score 574.2; DB 1; Length 590;
Best Local Similarity 99.5%; Pred. No. 0.13;
Matches 576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 268 CGGTCGACCGCGTGAACCCCGCCAGTCTGGCCCCCGTTCCCGAGTTTCTCTGCCGA 327
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Qy 580 CGGTTTACCGCGCTGGACCCCGCCAGTCTGGCCCCCGTTCCCGAGTTTCTCTGCCGA 521
Db |||||
Qy 328 TCTGGTCAACTGGGCCACACCTGGGTTCTGGCCATCACGGCCACCAACCGCGTGC 387
Db |||||
Qy 520 TCTGGTCAACTGGGCCACACCTGGGTTCTGGCCATCACGGCCACCAACCGCGTGC 461
Db |||||
Qy 388 CCGGGAGGGCGCGCCGAGCGGAGGCGGCGCCCGCCAGCCGACCTCCAAACCTCTCTCGT 447
Db |||||
Qy 460 CCGGGAGGGCGCGCCGAGCGGAGGCGGCGGCCCGCCAGCCGACCTCCAAACCTCTCTCGT 401
Db |||||
Qy 448 GGAACCAATATCTGGCATTTGAGCAGTTTCGCATTCCCGGGGACCGCTGTGGGCGGCAG 507
Db |||||
Qy 400 GGAACCAATATCTGGCATTTGAGCAGTTTCGCATTCCCGGGGACCGCTGTGGGCGGCAG 341
Db |||||
Qy 508 CCGGCCAGGGCTCTACAGCCATCTCTTGGACCGAGTCTATGAGCTGAACGTGTGCTCC 567
Db |||||
Qy 340 CCGGCCAGGGCTCTACAGCCATCTCTTGGACCGAGTCTATGAGCTGAACGTGTGCTCC 281
Db |||||
Qy 568 GACCGCGCGCTAGCCGCTGGGTGTCTCTTTTGGCCCGCCCGCCAGATGGCGCGCA 627
Db |||||
Qy 280 GACCGCGCGCTAGCCGCTGGGTGTCTCTTTTGGCCCGCCCGCCAGATGGCGCGCA 221
Db |||||
Qy 628 CATGCACATCATCATCAACCGCGAGGACATGGGCGCGAGCGCCCGGGGACTGCCAGCTGC 687
Db |||||
Qy 220 CATGCACATCATCATCAACCGCGAGGACATGGGCGCGAGCGCCCGGGGACTGCCAGCTGC 161
Db |||||

Qy 688 GCAGCCCCCTCTAGCGCGTGTGGAGCTGTTTCTCCACAAAGAGCGTGGCCTTGTCCA 747
Db |||||
Qy 160 GCAGCCCCCTCTAGCGCGTGTGGAGCTGTTTCTCCACAAAGAGCGTGGCCTTGTCCA 101
Db |||||
Qy 748 GCTCGAGTATGGCTTGGCCATCCCTGCAGACTCTGTGCCGCTAGTGATACAAAGGAGCAT 807
Db |||||
Qy 100 GCTCGAGTATGGCTTGGCCATCCCTGCAGACTCTGTGCCGCTAGTGATACAAAGGAGCAT 41
Db |||||
Qy 808 GGTGCACCGGCTGGCCATTGATGGGCTCCACCTGCCCAA 846
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Db |||||

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Job time : 3 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:22:53 ; Search time 1 Seconds
(without alignments)
3.480 Million cell updates/sec

Title: US-10-014-774-3
Perfect score: 970
Sequence: 1 cctgccctatggccgagaga.....acattgtgcagccaagac 970

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5
Searched: 3 seqs, 1794 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 970

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : us-10-014-774-3.sl.rng4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	970	100.0	970	1 AAA89044	Human muscle-speci
2	573	59.1	574	1 ACH90886	Human genome deriv
3	250	25.8	250	1 ABX75964	Human Neu4 cDNA.

ALIGNMENTS

RESULT 1
AAA89044
ID AAA89044 standard; cDNA; 970 BP.

XX AC AAA89044;
XX DT 05-MAR-2001 (first entry)
XX DE Human muscle-specific protein Ozz cDNA.
XX KW Ozz; human; muscle-specific protein; myogenesis; muscle damage;
KW galactosialidosis; myocardial infarction; angina; therapy; diagnosis;
KW Chromosome 20; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 20..877
XX FT /*tag= a
XX PN WO200066733-A1.
XX PD 09-NOV-2000.
XX PF 28-APR-2000; 2000WO-US011900.

XX 29-APR-1999; 99US-0131814P.
PR (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX D'azzo A, Bongiovanni A, Nastasi T;
XX WPI; 2001-007221/01.
XX P-PSDB; AAB19851.
PT Novel protein Ozz and nucleic acid encoding the protein involved in
PT development and function of muscle, useful as target for identifying
PT drugs effective in treating myogenesis disorders.
XX Claim 12; Fig 2B; 62pp; English.
XX The present sequence is that of cDNA encoding a novel human muscle-
CC specific protein, termed Ozz (see AAB19851), that regulates development
CC and function of muscle cells. The human Ozz gene was located on
CC chromosome 20 (PPGB locus). The cDNA shows 85% homology to murine Ozz
CC cDNA (see AAA89043). The murine Ozz protein is preferentially expressed
CC by a 1.0 kb mRNA in heart and skeletal muscle. Human and mouse proteins
CC share homology with neuralised proteins, which are associated with a
CC number of muscle proteins, including beta-catenin. Ozz protein is useful
CC for detecting damage to muscle tissue or disease associated with a defect
CC in Ozz expression. Increase in the level of Ozz protein in blood or in a
CC blood fraction indicates damage to muscle tissue in the heart and an
CC abnormal level or localization of Ozz in muscle cells from the atrium of
CC the heart of a subject is useful for detecting galactosialidosis
CC (claimed). The presence of Ozz in blood or a blood fraction indicates
CC muscle tissue damage e.g. ischaemia associated with either unstable
CC angina, myocardial infarction or both. Nucleotide sequences derived from
CC the gene encoding Ozz and peptide sequences derived from Ozz are useful
CC as targets to identify drugs that are effective in treating myogenesis
CC disorders
XX SQ Sequence 970 BP; 157 A; 345 C; 296 G; 172 T; 0 U; 0 Other;

Query Match 100.0%; Score 970; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGCCCTATGGCCGAGAGATGGCTGCTCCGAGCCCGTGGATTCCGGTGCACCTCTG 60
DB 1 CCTGCCCTATGGCCGAGAGATGGCTGCTCCGAGCCCGTGGATTCCGGTGCACCTCTG 60
QY 61 GGGACTCGAGCGCCGAGCGCCCTCCACCCGCTTCATCGGTGACGCGTCCCAACAT 120
DB 61 GGGACTCGAGCGCCGAGCGCCCTCCACCCGCTTCATCGGTGACGCGTCCCAACAT 120
QY 121 CCGGTGAGACCCCTCTGGGAGCGGGCCACACGCGTGGAGAGCTTCGCCACGCGGTGTG 180
DB 121 CCGGTGAGACCCCTCTGGGAGCGGGCCACACGCGTGGAGAGCTTCGCCACGCGGTGTG 180
QY 181 CTTACGCGCGAGCGCGTGGCCCGGGCCAGGCTTCTCTGTCGAGATCGAGGAGAAAGA 240
DB 181 CTTACGCGCGAGCGCGTGGCCCGGGCCAGGCTTCTCTGTCGAGATCGAGGAGAAAGA 240
QY 241 GCTGGGCTGGTGGGACATCTGCGTCTCGGTCTGACCCGCTGGACCCCGCCAGTCTGCG 300
DB 241 GCTGGGCTGGTGGGACATCTGCGTCTCGGTCTGACCCGCTGGACCCCGCCAGTCTGCG 300
QY 301 CCCCGTCCCGAGTTTCTCTGCCGATCTGGTCAACCTGGGCCACACCTGGGTCTTCGC 360
DB 301 CCCCGTCCCGAGTTTCTCTGCCGATCTGGTCAACCTGGGCCACACCTGGGTCTTCGC 360
QY 361 CATCAGCGCCACCAACACCGCGTCCCGGGAGGGCCCGCGAGGCGGAGGCGCGGC 420
DB 361 CATCAGCGCCACCAACACCGCGTCCCGGGAGGGCCCGCGAGGCGGAGGCGCGGC 420
QY 421 CCCAGCGGACCTCCAAACCCCTCTCGTGGAAACCATATCTGGCCATTGACGATTCGCAT 480
DB 421 CCCAGCGGACCTCCAAACCCCTCTCGTGGAAACCATATCTGGCCATTGACGATTCGCAT 480

Qy 609 GCCCGGATGACGCGGACATGACATCATCATCAACGCGGAGGACATGCGGCCGAGCG 668
 Db 421 GCGCGGATGACGCGGACATGACATCATCATCAACGCGGAGGACATGCGGCCGAGCG 480
 Qy 669 CCGCGGAGCTGCCAGCTGCGCAGCCCTCTACGCGGTGGTGGACGTGTGCTTCCCAA 728
 Db 481 CCGCGGAGCTGCCAGCTGCGCAGCCCTCTACGCGGTGGTGGACGTGTGCTTCCCAA 540
 Qy 729 AGACGCTGCGCTTGTCCAGCTCGAGTATGGCT 761
 Db 541 AGACGCTGCGCTTGTCCAGCTCGAGTATGGCT 573

RESULT 3
 ID ABX75864 standard; cDNA; 250 BP.
 AC
 XX
 XX
 XX
 DT 31-MAR-2003 (first entry)
 DE Human Neu4 cDNA.

Human; mouse; rat; gene; ss; neuralised polypeptide; Neu; NHR; cancer;
 neuralised homology repeat; C3HC4 RING-zinc finger domain; myogenesis;
 neurogenic function; transcriptional regulator; cell signalling; pain;
 calcium-signal transducer; synaptogenesis; memory learning; anxiety;
 tumorigenesis; organ development; central nervous system; depression;
 neurogenic gene; nuclear transport; Parkin-like protein; RNA processing;
 inductive tissue interaction; cytokine signalling; axonal path-finding;
 neurodegenerative disease; cytostatic; antidepressant; analgesic;
 tranquiliser; neuroprotective; Neu1; Neu2; Neu3; Neu4.

Homo sapiens.

US2002132293-A1.

19-SEP-2002.

14-MAR-2001; 2001US-00808387.

14-MAR-2001; 2001US-00808387.

(PALM/) PALM K.

(TIMM/) TIMMUSK T.

Palm K, Timmusk T;

WPI; 2003-174081/17.

P-PSDB; ABU56257.

Novel neuralized polypeptide, Neu useful for controlling cell proliferation and calcium signaling induced transcriptional processes and treating depression, pain, anxiety, cancer and neurodegenerative diseases.

Claim 6; Page 49; 75pp; English.

The invention relates to a purified neuralised (Neu) polypeptide comprising at least one neuralised homology repeat (NHR) domain and a C3HC4 RING-zinc finger domain, and a polynucleotide encoding the polypeptide. The polynucleotide is useful for constructing a transcribed host cell that expresses a Neu protein. Neu has neurogenic function and functions as a transcriptional regulator, as a calcium-signal transducer, in cell signalling and synaptogenesis, in memory learning, tumorigenesis, myogenesis and development of other organ systems and is related to repair and regeneration after injury to the central nervous system. Neu interacts with neurogenic genes, proteins implicated in nuclear transport and with Parkin-like proteins. Neu has the potential to interfere with inductive tissue interactions, cytokine signalling, RNA processing, early immediate responses, death of specific cell populations, nuclear hormone receptor signalling and axonal path-finding. The Neu family of proteins presents a set of diagnostic and therapeutic

CC targets, especially for treating cancer. Manipulating Neu expression and function is useful in controlling a variety of diseases including depression, pain, anxiety, neurodegenerative diseases and cancer.
 CC Sequences ABX75848-ABX75864 represent Neu polynucleotides of the invention
 CC
 XX Sequence 250 BP; 32 A; 88 C; 83 G; 47 T; 0 U; 0 Other;

Query Match 25.8%; Score 250; DB 1; Length 250;
 Best Local Similarity 100.0%; Pred. NO. 2.8;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 CGCTTCCATCGGGTGCAACGCGTGCACATCGCGGTGACCCCTCTGGAGCGGGCCACA 151
 Db 1 CGCTTCCATCGGGTGCAACGCGTGCACATCGCGGTGACCCCTCTGGAGCGGGCCACA 60
 Qy 152 CGGTGGAGAGCTTCGCCCAACGCGTGTCTTACGCGCGAGCGCGTGGCCCGGGCCAG 211
 Db 61 CGGTGGAGAGCTTCGCCCAACGCGTGTCTTACGCGCGAGCGCGTGGCCCGGGCCAG 120
 Qy 212 GTCTTCTCTGTCGAGATCGAGGAGAGAGCTGGGCTGGTGGGACATCTCGGTCTCGGT 271
 Db 121 GTCTTCTCTGTCGAGATCGAGGAGAGAGCTGGGCTGGTGGGACATCTCGGTCTCGGT 180
 Qy 272 CTGACCGCGTGGACCCCGCCAGTCTGGCCCCCGTTCGCCAGTCTTCTCTGCCGATCTG 331
 Db 181 CTGACCGCGTGGACCCCGCCAGTCTGGCCCCCGTTCGCCAGTCTTCTCTGCCGATCTG 240
 Qy 332 GTCAACCTGG 341
 Db 241 GTCAACCTGG 250

Search completed: March 2, 2006, 10:22:55
 Job time : 2 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:27:41 ; Search time 1 Seconds
(without alignments)
3.480 Million cell updates/sec

Title: US-10-014-774-3
Perfect score: 970
Sequence: 1 ccgcctatgagccgagaga.....acattgctgcagccagagac 970

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 3 seqs, 1794 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 970

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database: us-10-014-774-3.sl.rnpbms.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	970	100.0	970	1	US-10-014-774-3
2	573	59.1	574	1	US-10-029-386-24081
3	250	25.8	250	1	US-09-808-387-33

ALIGNMENTS

RESULT 1
US-10-014-774-3
Sequence 3, Application US/10014774
Publication No. US20020099173A1
GENERAL INFORMATION:
APPLICANT: D'Azzo, Alessandra
APPLICANT: Bongiovanni, Antonella
APPLICANT: Nascetti, Tommaso
TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle
FILE REFERENCE: 2427/1F509-US1
CURRENT APPLICATION NUMBER: US/10/014,774
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: PCT/US00/11900
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/131,814
PRIOR FILING DATE: 1999-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 970
TYPE: DNA
ORGANISM: Homo sapiens
US-10-014-774-3

Query Match 100.0%; Score 970; DB 1; Length 970;

Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	CTGECCTATGAGCCGAGAGATGCTGCTCCGAGCCCGTGGATTCGGGTGACACTG	60
QY	61	GGGACTGAGAGCCCGAGAGCCCTCCCAACCGCTTCATCGGGTGACAGGTGCAACAT	120
DB	61	GGGACTGAGAGCCCGAGAGCCCTCCCAACCGCTTCATCGGGTGACAGGTGCAACAT	120
QY	121	CCGCTGAGACCCCTCTGAGAGCGAGGACCAACGCGTGAAGCTTCGCTCAACGCGTGTG	180
DB	121	CCGCTGAGACCCCTCTGAGAGCGAGGACCAACGCGTGAAGCTTCGCTCAACGCGTGTG	180
QY	181	CTTACAGCCGAGAGCCGCTGAGCCCGGAGAGCTTCCTGCTGAGATTCGAGAGAAAGA	240
DB	181	CTTACAGCCGAGAGCCGCTGAGCCCGGAGAGCTTCCTGCTGAGATTCGAGAGAAAGA	240
QY	241	GCTGGGCTGAGCGGAGCATGCGGTGCTGCTGAGACGCGCTGAGACCCGCAAGCTGAC	300
DB	241	GCTGGGCTGAGCGGAGCATGCGGTGCTGCTGAGACGCGCTGAGACCCGCAAGCTGAC	300
QY	301	CCCGCTCCGAGTTTCTCTGCGAGATCTGATCAACTGAGGCCACACTGAGTCTTGC	360
DB	301	CCCGCTCCGAGTTTCTCTGCGAGATCTGATCAACTGAGGCCACACTGAGTCTTGC	360
QY	361	CATCAACGCGGACCAACACCGCGTGCCTCCGAGAGGCGCCCGGAGGCGAGGCGAGC	420
DB	361	CATCAACGCGGACCAACACCGCGTGCCTCCGAGAGGCGCCCGGAGGCGAGGCGAGC	420
QY	421	CCCGAGCCGAGCTCCCAACCTCTCTGAGAACATATCGGGCATTTGAGAGTTTGGAT	480
DB	421	CCCGAGCCGAGCTCCCAACCTCTCTGAGAACATATCGGGCATTTGAGAGTTTGGAT	480
QY	481	TCCCGGAGACGCGCTGAGGAGCGAGCGGACGAGCGGAGGAGGAGGAGGAGGAGG	540
DB	481	TCCCGGAGACGCGCTGAGGAGCGAGCGGACGAGCGGAGGAGGAGGAGGAGGAGG	540
QY	541	GCTCTATAGAGTGAACGTGCTGCTCCGAGCGCGCGTGAAGCCGCTGAGTGTCTCT	600
DB	541	GCTCTATAGAGTGAACGTGCTGCTCCGAGCGCGCGTGAAGCCGCTGAGTGTCTCT	600
QY	601	TTGCCCCGCGCCCATGAGCAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	660
DB	601	TTGCCCCGCGCCCATGAGCAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	660
QY	661	CCGAGCGCGCGGAGTGCAGCTGCGAGCGCCCTTACAGCGGTGAGAGGTGTTGC	720
DB	661	CCGAGCGCGCGGAGTGCAGCTGCGAGCGCCCTTACAGCGGTGAGAGGTGTTGC	720
QY	721	TTTCACAAAGAGCGTGCCTTGTCACTGAGTATGAGCTTTCATCTCCGAGACTCT	780
DB	721	TTTCACAAAGAGCGTGCCTTGTCACTGAGTATGAGCTTTCATCTCCGAGACTCT	780
QY	781	GTGCGGCTTATGATCAAAAGAGATGATGACCGGCTGAGGATTTGATGAGGCTCACT	840
DB	781	GTGCGGCTTATGATCAAAAGAGATGATGACCGGCTGAGGATTTGATGAGGCTCACT	840
QY	841	GGCCAAAGAACTTATGAGATTTCTGCAAGTATGAGTGAAGACCCAGAGTGCACAG	900
DB	841	GGCCAAAGAACTTATGAGATTTCTGCAAGTATGAGTGAAGACCCAGAGTGCACAG	900
QY	901	AGCTGATCTTGAAGCCGAGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
DB	901	AGCTGATCTTGAAGCCGAGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
QY	961	CAGCCAGAGC 970	
DB	961	CAGCCAGAGC 970	

RESULT 2

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US-10-029-386-24081
Sequence 24081, Application US/10029386
Publication NO. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24081
LENGTH: 574
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL008726.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: SWISSPROT HIT: P29503, EVALUE 1.30e-01
OTHER INFORMATION: NT HIT: G16679436, EVALUE 5.00e-29
OTHER INFORMATION: EST_HUMAN HIT: AW515245.1, EVALUE 0.00e+00
US-10-029-386-24081

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Query Match      59.1%; Score 573; DB 1; Length 574;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Oy	189	GCAGAGCCCTGAGCCCGGAGCCAGGCTTCTCTGAGATCGAGGAGAAAGCTGGGCT	248
Db	1	GCAGAGCCCTGAGCCCGGAGCCAGGCTTCTCTGAGATCGAGGAGAAAGCTGGGCT	60
Oy	249	GATGCGACATCTGCGTCTCGGTCTGACCGCGCTGGAACCCCGCAGTCTGCGCCCTTTC	308
Db	61	GATGCGACATCTGCGTCTCGGTCTGACCGCGCTGGAACCCCGCAGTCTGCGCCCTTTC	120
Oy	309	CCGAGTTTCTCTGCGGATCTGTGCAACTGTGGGCAACACTGGGTCTTTGCGCATCAGC	368
Db	121	CCGAGTTTCTCTGCGGATCTGTGCAACTGTGGGCAACACTGGGTCTTTGCGCATCAGC	180
Oy	369	GCCACCAACAACGCGTGGCCCGGGAGGGGCGGCGCGAGGCGAGCAGCGCCCAAGC	428
Db	181	GCCACCAACAACGCGTGGCCCGGGAGGGGCGGCGCGAGGCGAGCAGCGCCCAAGC	240
Oy	429	GACCTCCAACCTCTCTGAGAACCATATCTGCGCATTGAGCAGTTTCCCGGG	488
Db	241	GACCTCCAACCTCTCTGAGAACCATATCTGCGCATTGAGCAGTTTCCCGGG	300
Oy	489	ACCGCCTGATGGGCGGCAAGCGGCGCAAGGCTCTAACGCCATCTTTGAGCCAGCTTATG	548
Db	301	ACCGCCTGATGGGCGGCAAGCGGCGCAAGGCTCTAACGCCATCTTTGAGCCAGCTTATG	360
Oy	549	AGCTGAAGTGTGCTCCGACCGGCGGCGCGCTGAGCGCTGGGTCTCTTTGGCCGC	608
Db	361	AGCTGAAGTGTGCTCCGACCGGCGGCGCGCTGAGCGCTGGGTCTCTTTGGCCGC	420
Oy	609	GCCCCGATGGCAAGCGCCGACATGACATCATCATCAACGCGAGGACATGGGCGGAGCG	668
Db	421	GCCCCGATGGCAAGCGCCGACATGACATCATCATCAACGCGAGGACATGGGCGGAGCG	480
Oy	669	CCCGGGGACTGCACTGCGCAAGCCCTTCAACGCGGTGGTGACGTTTGTCTCAACA	728
Db	481	CCCGGGGACTGCACTGCGCAAGCCCTTCAACGCGGTGGTGACGTTTGTCTCAACA	540
Oy	729	AGAGCGTGCCTTGTCCAGCTCGAGTATAGCT	761
Db	541	AGAGCGTGCCTTGTCCAGCTCGAGTATAGCT	573

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: Sequence 33, Application US/09808387
: Patent No. US20020132293A1
: GENERAL INFORMATION
: APPLICANT: Kata Palm
: APPLICANT: Tonis Tiimusk
: APPLICANT: Cemines Research
: TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
: TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
: FILE REFERENCE: CEMINES.001A
: CURRENT APPLICATION NUMBER: US/09/808,387
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 33
: LENGTH: 250
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-808-387-33

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Query Match	25.8%;	Score 250;	DB 1;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 2.8;		
Matches 250;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	92	CGCTTCATCGGGTGCACGGATGCTCAACATCCGGTGAACCCCTCTGGGACGGCGGGCCACA	158
Db	1	CGCTTCATCGGGTGCACGGATGCTCAACATCCGGTGAACCCCTCTGGGACGGCGGGCCACA	60
Oy	152	CGCGTGAAGACTTGCGCCACCGGCGTGTGCTTCAAGCCGCGAGCCGGCTGCGCCCGGGGACAG	211
Db	61	CGCGTGAAGACTTGCGCCACCGGCGTGTGCTTCAAGCCGCGAGCCGGCTGCGCCCGGGGACAG	120
Oy	212	GTCCTTCCTGGTCGAGATCAGAGAGAAAGCTGGGCTGTGTCGAGACATCTGCTCGGT	271
Db	121	GTCCTTCCTGGTCGAGATCAGAGAGAAAGCTGGGCTGTGTCGAGACATCTGCTCGGT	180
Oy	272	CTGACCGCGCTGAGACCCCGCCAGTGTGGCCCCGTTCCGAGTTTCTCTGACCAGATCTG	331
Db	181	CTGACCGCGCTGAGACCCCGCCAGTGTGGCCCCGTTCCGAGTTTCTCTGACCAGATCTG	240
Oy	332	GTCACCTGG	341
Db	241	GTCACCTGG	250

Search completed: March 2, 2006, 10:27:43
Job time : 1 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 10:29:19 ; Search time 0.001 Seconds
(without alignments)
787.640 Million cell updates/sec

Title: US-10-014-774-3
Perfect score: 970
Sequence: 1 cctgcctatggcgcagaga.....acattgtccagcaagac 970

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 17 seqs, 406 residues

Total number of hits satisfying chosen parameters: 34

Minimum DB seq length: 0
Maximum DB seq length: 970

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 17 summaries

Database : us-10-014-774-3.sl.rnpbn4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	25	2.6	25	1	US-11-121-849-260796 Sequence 260796,
2	25	2.6	25	1	US-11-121-849-260797 Sequence 260797,
3	25	2.6	25	1	US-11-121-849-260798 Sequence 260798,
4	25	2.6	25	1	US-11-121-849-260799 Sequence 260799,
5	25	2.6	25	1	US-11-121-849-260800 Sequence 260800,
6	25	2.6	25	1	US-11-121-849-260801 Sequence 260801,
7	25	2.6	25	1	US-11-121-849-260802 Sequence 260802,
8	25	2.6	25	1	US-11-121-849-260803 Sequence 260803,
9	25	2.6	25	1	US-11-121-849-260804 Sequence 260804,
10	25	2.6	25	1	US-11-121-849-260805 Sequence 260805,
11	25	2.6	25	1	US-11-121-849-260806 Sequence 260806,
C 12	23	2.4	23	1	US-10-310-914A-470229 Sequence 470229,
C 13	23	2.4	23	1	US-10-310-914A-470237 Sequence 470237,
C 14	22	2.3	22	1	US-10-310-914A-470239 Sequence 470239,
C 15	21	2.2	21	1	US-10-310-914A-470228 Sequence 470228,
C 16	21	2.2	21	1	US-10-310-914A-470236 Sequence 470236,
C 17	21	2.2	21	1	US-10-310-914A-470238 Sequence 470238,

ALIGNMENTS

RESULT 1
US-11-121-849-260796
; Sequence 260796, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260796
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260796

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1; Indels 0;
Matches 25; Conservative 0; Mismatches 0; Gaps 0;
Qy 630 TGCACATCATCATCAACGGCGGAGGA 654
Db 1 TGCACATCATCATCAACGGCGGAGGA 25

RESULT 2
US-11-121-849-260797
; Sequence 260797, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260797
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260797

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1; Indels 0;
Matches 25; Conservative 0; Mismatches 0; Gaps 0;
Qy 641 ATCAACGGCGGAGGACATGGGCCCGA 665
Db 1 ATCAACGGCGGAGGACATGGGCCCGA 25

RESULT 3
US-11-121-849-260798
; Sequence 260798, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260798
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260798

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1; Indels 0;
Matches 25; Conservative 0; Mismatches 0; Gaps 0;

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QY 693 CCCTCTACGGCTGGTGGAGGTGT 717
Db 1 CCCTCTACGGCTGGTGGAGGTGT 25

RESULT 4
US-11-121-849-260799
; Sequence 260799, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260799
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260799

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 TTGCTTCCACAAAGAGCGTGGCCT 741
Db 1 TTGCTTCCACAAAGAGCGTGGCCT 25

RESULT 5
US-11-121-849-260800
; Sequence 260800, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260800
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260800

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 TGGCCCTTGTCAGCTCGAGTATGG 759
Db 1 TGGCCCTTGTCAGCTCGAGTATGG 25

RESULT 6
US-11-121-849-260801
; Sequence 260801, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
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; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260801
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260801

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 TATGAGCTGAACGTGCTGCTCCGA 569
Db 1 TATGAGCTGAACGTGCTGCTCCGA 25

RESULT 7
US-11-121-849-260802
; Sequence 260802, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260802

Query Match 2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 771 TGCAGACTCTGCGCGCTAGTGAT 795
Db 1 TGCAGACTCTGCGCGCTAGTGAT 25

RESULT 8
US-11-121-849-260803
; Sequence 260803, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260803
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260803
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Query Match      2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 777 CTCTGTCCGCGCTAGTGATACAAAG 801
Db 1 CTCTGTCCGCGCTAGTGATACAAAG 25

RESULT 9
US-11-121-849-260804
; Sequence 260804, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260804
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260804

Query Match      2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 794 ATACAAAGGAGCATGTGTCACCGGC 818
Db 1 ATACAAAGGAGCATGTGTCACCGGC 25

RESULT 10
US-11-121-849-260805
; Sequence 260805, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260805
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260805

Query Match      2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 GCCGTAGCCGCTGGTGTCCTT 600
Db 1 GCCGTAGCCGCTGGTGTCCTT 25

RESULT 11
US-11-121-849-260806
; Sequence 260806, Application US/11121849
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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 260806
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-260806

Query Match      2.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 ATGCGACGGCGCATGTCACATCAT 639
Db 1 ATGCGACGGCGCATGTCACATCAT 25

RESULT 12
US-10-310-914A-470229/C
; Sequence 470229, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470229
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-470229

Query Match      2.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 890 CACCAGAGCACAGCTGTCATCTG 912
Db 23 CACCAGAGCACAGCTGTCATCTG 1

RESULT 13
US-10-310-914A-470237/C
; Sequence 470237, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470237
; LENGTH: 23
; TYPE: RNA
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; ORGANISM: Human
US-10-310-914A-470237

Query Match 2.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 941 GAAGTTGCCACATGCTGCCAG 963
|||||
Db 23 GAAGTTGCCACATGCTGCCAG 1

RESULT 14

US-10-310-914A-470239/c
; Sequence 470239, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kruzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 470239

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-470239

Query Match 2.3%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 947 GGCCACATGCTGCCAGCCAG 968
|||||
Db 22 GGCCACATGCTGCCAGCCAG 1

RESULT 15

US-10-310-914A-470228/c

; Sequence 470228, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kruzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 470228

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-470228

Query Match 2.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 892 CCAGAGCACAGCTGCATCCTG 912
|||||
Db 21 CCAGAGCACAGCTGCATCCTG 1

RESULT 16

US-10-310-914A-470236/c

; Sequence 470236, Application US/10310914A

; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470236
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-470236

Query Match 2.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 943 AGTTGCCACATGCTGCCAG 963
|||||
Db 21 AGTTGCCACATGCTGCCAG 1

RESULT 17

US-10-310-914A-470238/c

; Sequence 470238, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kruzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 470238

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-470238

Query Match 2.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 CCACAGTGCACACAGACACAG 902
|||||
Db 21 CCACAGTGCACACAGACACAG 1

Search completed: March 2, 2006, 10:29:20
Job time : 1 secs